

Status: Path 1 of [Dialog Information Services via Modem]

Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 3106900061...Open

DIALOG INFORMATION SERVICES

PLEASE LOGON:

***** HHHHHHHH SSSSSSSS?

Status: Signing onto Dialog

ENTER PASSWORD:

***** HHHHHHHH SSSSSSSS? *****

Welcome to DIALOG

Status: Connected

Dialog level 01.07.09D

Last logoff: 11aug01 14:05:03

Logon file001 12aug01 10:28:28

*** ANNOUNCEMENT ***

--Important Notice to Freelance Authors--

See HELP FREELANCE for more information

NEW FILE RELEASED

***EIU Business Magazines (File 622)

***IBISWorld Market Research (File 753)

***Investext PDF Index (File 745)

***Daily and Sunday Telegraph (London) Papers (File 756)

***The Mirror Group Publications (United Kingdom) (File 757)

UPDATING RESUMED

***Delphes European Business (File 481)

***Books In Print (File 470)

RELOADED

***Kompass Middle East/Africa/Mediterranean (File 585)

***Kompass Asia/Pacific (File 592)

***Kompass Central/Eastern Europe (File 593)

***Kompass Canada (File 594)

***CANCERLIT (File 159)

***Information Science Abstracts (File 202)

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broad spectrum of news wires.

>>> Enter BEGIN HOMEBASE for Dialog Announcements <<<

>>> of new databases, price changes, etc. <<<

KWIC is set to 50.

HIGHLIGHT set on as '*'

*** F222 is temporarily unavailable ***

File 1:ERIC 1966-2001/Aug 06
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Set	Items	Description
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?b 434, 5, 155

12aug01 10:28:32	User259980	Session D144.1
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\$0.23	0.065	DialUnits File1
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\$0.23		Estimated cost File1
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\$0.23		Estimated cost this search
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\$0.23		Estimated total session cost 0.065 DialUnits
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SYSTEM:OS - DIALOG OneSearch
 File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
 (c) 1998 Inst for Sci Info
 File 5:Biosis Previews(R) 1969-2001/Aug W1
 (c) 2001 BIOSIS
 File 155:MEDLINE(R) 1966-2001/Sep W1

Set Items Description
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 ?e au=ueki

Ref	Items	Index-term
E1	1	AU=UEKERT S
E2	1	AU=UEKESA T
E3	9	*AU=UEKI
E4	320	AU=UEKI A
E5	2	AU=UEKI AKIHARU
E6	12	AU=UEKI AKINORI
E7	1	AU=UEKI AKIO
E8	1	AU=UEKI AKIR
E9	28	AU=UEKI AKIRA
E10	6	AU=UEKI ATSUKO
E11	1	AU=UEKI ATSUSHI
E12	1	AU=UEKI ATUKO

Enter P or PAGE for more
 ?p

Ref	Items	Index-term
E13	22	AU=UEKI AYAKO
E14	2	AU=UEKI BH
E15	2	AU=UEKI E
E16	1	AU=UEKI F
E17	580	AU=UEKI H
E18	1	AU=UEKI HIDEAKI
E19	2	AU=UEKI HIDENORI
E20	26	AU=UEKI HIROAKI
E21	4	AU=UEKI HIROFUMI
E22	3	AU=UEKI HIRONORI
E23	18	AU=UEKI HIROSHI
E24	70	AU=UEKI I

Enter P or PAGE for more
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Ref	Items	Index-term
E25	38	AU=UEKI I F
E26	64	AU=UEKI IF
E27	2	AU=UEKI IORI
E28	1	AU=UEKI IR
E29	4	AU=UEKI IRIS
E30	12	AU=UEKI IRIS F
E31	89	AU=UEKI J
E32	4	AU=UEKI JUICHI
E33	8	AU=UEKI JUN
E34	3	AU=UEKI JUN-ICHI
E35	1	AU=UEKI JUNICHI
E36	468	AU=UEKI K

Enter P or PAGE for more
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Ref	Items	Index-term
E37	5	AU=UEKI KATSUJI
E38	9	AU=UEKI KAZUE
E39	2	AU=UEKI KAZUKO
E40	2	AU=UEKI KAZUYA
E41	1	AU=UEKI KEI
E42	39	AU=UEKI KEISUKE

E43	22	AU=UEKI KEN
E44	1	AU=UEKI KENJI
E45	1	AU=UEKI KEU
E46	1	AU=UEKI KOHICHI
E47	31	AU=UEKI KOHJIRO
E48	1	AU=UEKI KOICHIRO

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Ref	Items	Index-term
E49	1	AU=UEKI KOJHIRO
E50	2	AU=UEKI KOJIRO

?p

Ref	Items	Index-term
E1	2	AU=UEKI KOJIRO
E2	3	AU=UEKI KOJIROH
E3	1	AU=UEKI KOUBUN
E4	2	AU=UEKI KOUICHIROU
E5	2	AU=UEKI KUNIKAZU
E6	1	AU=UEKI KUNIMASA
E7	3	AU=UEKI KYO
E8	2	AU=UEKI KYOKO
E9	418	AU=UEKI M
E10	6	AU=UEKI MAKOTO
E11	33	AU=UEKI MASAACK
E12	1	AU=UEKI MASAKAI

Enter P or PAGE for more

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Ref	Items	Index-term
E13	1	AU=UEKI MASAKI
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E15	11	AU=UEKI MASASHI
E16	6	AU=UEKI MASATO
E17	1	AU=UEKI MASAYA
E18	1	AU=UEKI MAYUMI
E19	2	AU=UEKI MICHIKO
E20	54	AU=UEKI MINORU
E21	1	AU=UEKI MISUZU
E22	3	AU=UEKI MITSUHIKO
E23	61	AU=UEKI N
E24	8	AU=UEKI NOBORU

Enter P or PAGE for more

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E25	9	AU=UEKI NOBUHIDE
E26	1	AU=UEKI NORITAKA
E27	2	AU=UEKI NORIYUKI
E28	35	AU=UEKI O
E29	5	AU=UEKI OSAMU
E30	30	AU=UEKI R
E31	1	AU=UEKI REIKO
E32	3	AU=UEKI RIE
E33	2	AU=UEKI RYUSUKE
E34	990	AU=UEKI S
E35	1	AU=UEKI S S
E36	2	AU=UEKI S Y M

Enter P or PAGE for more

?s e25

S1	9	AU="UEKI NOBUHIDE"
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?rd

...completed examining records

S2	9	RD (unique items)
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?t/3/all

2/3/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

12500720 BIOSIS NO.: 200000254222
Identification and characterization of human ZNF274 cDNA, which encodes a novel Kruppel-type zinc-finger protein having nucleolar targeting ability.
AUTHOR: Yano Kazuhiro; *Ueki Nobuhide*; Oda Tamaki; Seki Naohiko; Masuho Yasuhiko; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Biological Technology Laboratory, Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-0812**Japan
JOURNAL: Genomics 65 (1):p75-80 April 1, 2000
MEDIUM: print.
ISSN: 0888-7543
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

2/3/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

12369624 BIOSIS NO.: 200000123126
cDNA cloning of a novel human gene NAKAP95, neighbor of A-kinase anchoring protein 95 (AKAP95) on chromosome 19p13.11-p13.12 region.
AUTHOR: Seki Naohiko; *Ueki Nobuhide*; Yano Kazuhiro; Saito Toshiyuki; Masuho Yasuhiko; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-0812**Japan
JOURNAL: Journal of Human Genetics 45 (1):p31-37 2000
ISSN: 1434-5161
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

2/3/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

12147353 BIOSIS NO.: 199900442202
Isolation, tissue expression, and chromosomal assignment of a human LIM protein gene, showing homology to rat Enigma homologue (ENH).
AUTHOR: *Ueki Nobuhide*; Seki Naohiko; Yano Kazuhiro; Masuho Yasuhiko; Saito Toshiyuki; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Biological Technology Laboratory, Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-0812**Japan
JOURNAL: Journal of Human Genetics 44 (4):p256-260 1999
ISSN: 1434-5161
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

2/3/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

11994216 BIOSIS NO.: 199900274735
Isolation and characterization of a novel human gene (HFB30) which encodes a protein with a RING finger motif.
AUTHOR: *Ueki Nobuhide*; Seki Naohiko; Yano Kazuhiro; Masuho Yasuhiko; Saito Toshiyuki; Muramatsu Masa-aki(a
AUTHOR ADDRESS: (a)Biological Technology Laboratory, Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-08**Japan
JOURNAL: Biochimica et Biophysica Acta 1445 (2):p232-236 May 14, 1999

ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

2/3/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

11949082 BIOSIS NO.: 199900195191
Isolation and chromosomal assignment of human genes encoding cofactor of LIM homeodomain proteins, CLIM1 and CLIM2.
AUTHOR: *Ueki Nobuhide*; Seki Naohiko; Yano Kazuhiro; Ohira Miki; Saito Toshiyuki; Masuho Yasuhiko; Muramatsu Masa-aki(a)
AUTHOR ADDRESS: (a)Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba, 292-0812**Japan
JOURNAL: Journal of Human Genetics 44 (2):p112-115 1999
ISSN: 1434-5161
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

2/3/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11793329 BIOSIS NO.: 199900039438
Selection system for genes encoding nuclear-targeted proteins.
AUTHOR: *Ueki Nobuhide*(a); Oda Tamaki; Kondo Maiko; Yano Kazuhiro; Noguchi Teruhisa; Muramatsu Masa-Aki
AUTHOR ADDRESS: (a)Biological Technol. Lab., Helix Res. Inst., Kisarazu-shi, Chiba 292-0812**Japan
JOURNAL: Nature Biotechnology 16 (13):p1338-1342 Dec., 1998
ISSN: 1087-0156
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

2/3/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11770540 BIOSIS NO.: 199900016649
NOLP: Identification of a novel human nucleolar protein and determination of sequence requirements for its nucleolar localization.
AUTHOR: *Ueki Nobuhide*(a); Kondo Maiko; Seki Naohiko; Yano Kazuhiro; Oda Tamaki; Masuho Yasuhiko; Muramatsu Masa-Aki
AUTHOR ADDRESS: (a)Pharmaceuticals Discovery Laboratory, Mitsubishi Chemical Corporation, Kamoshida-cho 1000, Aobu-**Japan
JOURNAL: Biochemical and Biophysical Research Communications 252 (1):p 97-102 Nov. 9, 1998
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

2/3/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11266466 BIOSIS NO.: 199800047798
Recombinant thermostable cycloinulo-oligosaccharide fructanotransferase produced by Saccharomyces cerevisiae.
AUTHOR: Kanai Tamotsu; *Ueki Nobuhide*; Kawaguchi Tomoko; Teranishi Yutaka; Atomi Haruyuki; Tomorbaatar Chishignjamchuugjin; Ueda Mitsuyoshi; Tanaka Atsuo(a)

AUTHOR ADDRESS: (a)Lab. Applied Biological Chem., Dep. Synthetic Chem.
Biological Chem., Graduate Sch. Engineering,**Japan
JOURNAL: Applied and Environmental Microbiology 63 (12):p4956-4960 Dec.,
1997
ISSN: 0099-2240
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

2/3/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08996755 BIOSIS NO.: 199497005125
Distribution of bent DNA structures in the fission yeast centromere.
AUTHOR: *Ueki Nobuhide*; Momoi Hiroyuki; Yamada Hisami; Mizuno Takeshi(a
AUTHOR ADDRESS: (a)Lab. Mol. Microbiol., Sch. Agric., Nagoya Univ.,
Chikusa-ku, Nagoya 464**Japan
JOURNAL: Gene (Amsterdam) 132 (2):p247-250 1993
ISSN: 0378-1119
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

?s lexa(s)nuclear(w)localization(w)signal
2114 LEXA
438217 NUCLEAR
297004 LOCALIZATION
343956 SIGNAL
S3 3 LEXA(S)NUCLEAR(W)LOCALIZATION(W)SIGNAL
?rd
...completed examining records
S4 2 RD (unique items)
?t/9/all

4/9/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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12639445 BIOSIS NO.: 200000392947
A genetic system for detection of protein nuclear import and export.
AUTHOR: Rhee Yoon; Gurel Filiz; Gafni Yedidya; Dingwall Colin; Citovsky
Vitaly(a)
AUTHOR ADDRESS: (a)Department of Biochemistry and Cell Biology, Institute
for Cell and Development Biology, State University of New York, Stony
Brook, NY, 11794-5215**USA
JOURNAL: Nature Biotechnology 18 (4):p433-437 April, 2000
MEDIUM: print
ISSN: 1087-0156
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: We have developed a simple genetic assay to detect active nuclear
localization (NLS) and export signals (NES) on the basis of their
function within yeast cells. The bacterial LexA protein was modified
(mLexA) to abolish its intrinsic NLS and fused to the activation domain
of the yeast Gal4p (Gal4AD) with or without the SV40 large T-antigen NLS.
In the import assay, if a tested protein fused to mLexA-Gal4AD contains a
functional NLS, it will enter the cell nucleus and activate the reporter
gene expression. In the export assay, if a tested protein fused to
mLexA-SV40 NLS-Gal4AD contains a functional NES, it will exit into the
cytoplasm, decreasing the reporter gene expression. We tested this system
with known NLS and NES and then used it to demonstrate a NES activity of
the capsid protein of a plant geminivirus. This approach may help to
identify, analyze, and select for proteins containing functional NLS and
NES.

DESCRIPTORS:

MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular

Biophysics); Methods and Techniques
 BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae; Geminivirus--Plant
 Viruses, Viruses, Microorganisms; Rhizobiaceae--Gram-Negative Aerobic
 Rods and Cocci, Eubacteria, Bacteria, Microorganisms
 ORGANISMS: Agrobacterium (Rhizobiaceae); Saccharomyces cerevisiae
 (Ascomycetes)--strain-L40; geminivirus (Geminivirus)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Fungi;
 Microorganisms; Nonvascular Plants; Plant Viruses; Plants; Viruses
 CHEMICALS & BIOCHEMICALS: *LexA* protein--nuclear export, nuclear
 export signal, nuclear import, *nuclear* *localization* *signal*;
 nucleotoplasmic shuttle protein
 METHODS & EQUIPMENT: PCR {polymerase chain reaction}--DNA amplification,
 amplification method, in-situ recombinant gene expression detection,
 sequencing techniques; Transformer site-directed mutagenesis kit--
 Clontech, laboratory equipment; nuclear export assay--
 Bioassays/Physiological Analysis, analytical method; nuclear import
 assay--Bioassays/Physiological Analysis, analytical method
 CONCEPT CODES:
 03502 Genetics and Cytogenetics-General
 03504 Genetics and Cytogenetics-Plant
 10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
 31000 Physiology and Biochemistry of Bacteria
 31500 Genetics of Bacteria and Viruses
 33508 Virology-Plant Host Viruses
 BIOSYSTEMATIC CODES:
 02816 Geminivirus (1993-)
 06509 Rhizobiaceae (1992-)
 15100 Ascomycetes

4/9/2 (Item 2 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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09503679 BIOSIS NO.: 199497512049
 Sry is a transcriptional activator.
 AUTHOR: Dubin Robert A(a); Ostrer Harry
 AUTHOR ADDRESS: (a)Human Genetics Program, New York Univ. Med. Cent., 550
 First Ave., MSB 136, New York, NY 10016*USA
 JOURNAL: Molecular Endocrinology 8 (9):p1182-1192 1994
 ISSN: 0888-8809
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: The SRY gene functions as a genetic switch in gonadal ridge
 initiating testis determination. The mouse Sry and human SRY open reading
 frames (ORFs) share a conserved DNA-binding domain (the HMG-box) yet
 exhibit no additional homology outside this region. As judged by the
 accumulation of lacZ-SRY hybrid proteins in the nucleus, both the human
 and mouse SRY ORFs contain a *nuclear* *localization* *signal*. The mouse
 Sry HMG-box domain selectively binds the sequence NACAAT in vitro when
 challenged with a random pool of oligonucleotides and binds AACAAAT with
 the highest affinity. When put under the control of a heterologous
 promoter, the mouse Sry gene activated transcription of a reporter gene
 containing multiple copies of the AACAAAT binding site. Activation was
 likewise observed for a GAL4-responsive reporter gene, when the mouse Sry
 gene was linked to the DNA-binding domain of GAL4. Using this system, the
 activation function was mapped to a glutamine/histidine-rich domain. In
 addition, *LexA*-mouse Sry fusion genes activated a *LexA*-responsive
 reporter gene in yeast. In contrast, a GAL4-human SRY fusion gene did not
 cause transcriptional activation. These studies suggest that both the
 human and the mouse SRY ORFs encode nuclear, DNA-binding proteins and
 that the mouse Sry ORF can function as a transcriptional activator with
 separable DNA-binding and activator domains.

REGISTRY NUMBERS: 56-85-9: GLUTAMINE; 71-00-1: HISTIDINE
 DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology;
 Endocrine System (Chemical Coordination and Homeostasis); Genetics;
 Metabolism; Molecular Genetics (Biochemistry and Molecular Biophysics);

Physiology; Reproductive System (Reproduction)
 BIOSYSTEMATIC NAMES: Fungi-Unspecified--Fungi, Plantae; Hominidae--
 Primates, Mammalia, Vertebrata, Chordata, Animalia; Muridae--Rodentia,
 Mammalia, Vertebrata, Chordata, Animalia
 ORGANISMS: fungi (Fungi - Unspecified); human (Hominidae); mouse
 (Muridae); yeast (Fungi - Unspecified)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; fungi;
 humans; mammals; microorganisms; nonhuman mammals; nonhuman vertebrates
 ; nonvascular plants; plants; primates; rodents; vertebrates
 CHEMICALS & BIOCHEMICALS: GLUTAMINE; HISTIDINE
 MOLECULAR SEQUENCE DATABANK NUMBER: molecular sequence data
 MISCELLANEOUS TERMS: ACTIVATOR DOMAIN; DNA-BINDING DOMAIN; GAL4 -
 RESPONSIVE REPORTER GENE; GENETIC SWITCH; GLUTAMINE/HISTIDINE-RICH
 DOMAIN; GONADAL RIDGE; HMG-BOX; HOMOLOGY; LACZ-SRY HYBRID PROTEIN;
 LEXA-RESPONSIVE REPORTER GENE; NUCLEAR LOCALIZATION SIGNAL; NUCLEOTIDE
 SEQUENCE DATA; OPEN READING FRAME; TESTIS
 CONCEPT CODES:
 02506 Cytology and Cytochemistry-Animal
 02508 Cytology and Cytochemistry-Human
 03504 Genetics and Cytochemistry-Plant
 03506 Genetics and Cytochemistry-Animal
 03508 Genetics and Cytochemistry-Human
 10010 Comparative Biochemistry, General
 10300 Replication, Transcription, Translation
 10506 Biophysics-Molecular Properties and Macromolecules
 12003 Physiology, General and Miscellaneous-Comparative (1970-)
 13012 Metabolism-Proteins, Peptides and Amino Acids
 13014 Metabolism-Nucleic Acids, Purines and Pyrimidines
 16504 Reproductive System-Physiology and Biochemistry
 17006 Endocrine System-Gonads and Placenta
 51522 Plant Physiology, Biochemistry and Biophysics-Chemical
 Constituents
 10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
 10064 Biochemical Studies-Proteins, Peptides and Amino Acids
 BIOSYSTEMATIC CODES:
 15000 Fungi-Unspecified
 86215 Hominidae
 86375 Muridae
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 438217 NUCLEAR
 297004 LOCALIZATION
 343956 SIGNAL
 1249469 IDENTIF?
 S5 124 NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?
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 ...examined 50 records (100)
 ...completed examining records
 S6 71 RD (unique items)
 ?t/9/1-5

 6/9/1 (Item 1 from file: 434)
 DIALOG(R)File 434:SciSearch(R) Cited Ref Sci
 (c) 1998 Inst for Sci Info. All rts. reserv.

 06724313 Genuine Article#: ARZ48 Number of References: 36
 Title: *IDENTIFICATION* OF A *NUCLEAR*-*LOCALIZATION* *SIGNAL* OF A YEAST
 RIBOSOMAL-PROTEIN
 Author(s): MORELAND RB; NAM HG; HEREFORD LM; FRIED HM
 Corporate Source: UNIV N CAROLINA,DEPT BIOCHEM & NUTR/CHAPEL HILL//NC/27514
 ; UNIV N CAROLINA,DEPT CHEM/CHAPEL HILL//NC/27514; HARVARD UNIV,SCH
 MED,DANA FARBER CANC INST/BOSTON//MA/02115; HARVARD UNIV,SCH MED,DEPT
 MICROBIOL & GENET/BOSTON//MA/02115
 Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED
 STATES OF AMERICA, 1985, V82, N19, P6561-6565
 Language: ENGLISH Document Type: ARTICLE
 Geographic Location: USA
 Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences
 Journal Subject Category: MULTIDISCIPLINARY SCIENCES
 Research Fronts: 85-2737 002 (GENE EXPRESSION AND OTHER CHARACTERIZATION
 STUDIES OF THE SYNTHESIS AND SECRETION OF CELL MEMBRANE PROTEINS AND

GLYCOPROTEINS)
 85-4880 002 (UPTAKE AND ACCUMULATION OF VARIOUS PROTEINS BY THE CELL
 NUCLEUS)
 85-1468 001 (IDENTIFICATION, EXPRESSION AND OTHER ANALYSES OF GENES
 FROM ESCHERICHIA-COLI K-12 MUTANTS)
 85-4047 001 (CONFORMATIONAL AND STRUCTURAL STUDIES OF PEPTIDES AND
 PROTEINS)

Cited References:

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 MAGER WH, 1975, V402, P105, BIOCHIM BIOPHYS ACTA
 MANDECKI W, 1981, V147, P694, J BACTERIOL
 MEYUHAS O, 1980, V10, P113, GENE
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 SABATINI DD, 1982, V92, P1, J CELL BIOL
 SCHULTZ LD, 1983, V155, P8, J BACTERIOL
 SILVER PA, 1984, V81, P5951, P NATL ACAD SCI USA
 TEEM JL, 1984, V12, P8295, NUCLEIC ACIDS RES
 TEEM JL, 1983, THESIS BRANDEIS U WA
 WALTER P, 1984, V38, P5, CELL
 WARNER JR, 1977, V11, P201, CELL
 WARNER JR, 1985, V5, P1512, MOL CELL BIOL
 WARNER JR, 1980, P889, RIBOSOMES STRUCTURE
 WU RS, 1971, V51, P643, J CELL BIOL
 WUNDERLICH F, 1972, V7, P220, J MEMBRANE BIOL

6/9/2 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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13129833 BIOSIS NO.: 200100336982
 HIV-1 infection requires a functional integrase NLS.
 AUTHOR: Bouyac-Bertoia Michele; Dvorin Jeffrey D; Fouchier Ron A M; Jenkins
 Yonchu; Meyer Barbara E; Wu Lily I; Emerman Michael; Malim Michael H(a)
 AUTHOR ADDRESS: (a)Department of Microbiology, University of Pennsylvania
 School of Medicine, Philadelphia, PA, 19104: malim@mail.med.upenn.edu**
 USA
 JOURNAL: Molecular Cell 7 (5):p1025-1035 May, 2001
 MEDIUM: print
 ISSN: 1097-2765
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English
 SUMMARY LANGUAGE: English

ABSTRACT: HIV-1 is able to infect nondividing cells productively in part
 because the postentry viral nucleoprotein complexes are actively imported
 into the nucleus. In this manuscript, we *identify* a novel *nuclear*
 localization *signal* (NLS) in the viral integrase (IN) protein that is
 essential for virus replication in both dividing and non-dividing cells.
 The IN NLS stimulates the efficient nuclear accumulation of viral DNA as

well as virion-derived IN protein during the initial stages of infection but is dispensable for catalytic function. Because this NLS is required for infection irrespective of target cell proliferation, we suggest that interactions between uncoated viral nucleoprotein complexes and the host cell nuclear import machinery are critical for HIV-1 infection of all cells.

DESCRIPTORS:

MAJOR CONCEPTS: Enzymology (Biochemistry and Molecular Biophysics); Cell Biology; Infection
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae--Animal Viruses, Viruses, Microorganisms
ORGANISMS: HIV-1 {human immunodeficiency virus 1} (Retroviridae); human (Hominidae)--in vitro cell lines
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses
DISEASES: HIV-1 infection {human immunodeficiency virus 1 infection}--immune system disease, viral disease
CHEMICALS & BIOCHEMICALS: functional integrase NLS {functional integrase nuclear localization signal}; viral integrase protein
METHODS & EQUIPMENT: Western blotting--detection/labeling techniques, gene mapping; indirect immunofluorescence--detection/labeling techniques

ALTERNATE INDEXING: HIV Infections (MeSH)

CONCEPT CODES:

02502 Cytology and Cytochemistry-General
02508 Cytology and Cytochemistry-Human
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10802 Enzymes-General and Comparative Studies; Coenzymes
33506 Virology-Animal Host Viruses
34508 Immunology and Immunochemistry-Immunopathology, Tissue Immunology
36006 Medical and Clinical Microbiology-Virology

BIOSYSTEMATIC CODES:

02623 Retroviridae (1993-)
86215 Hominidae

6/9/3 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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13127712 BIOSIS NO.: 200100334861

Nuclear import and DNA-binding activity of RFX1. Evidence for an autoinhibitory mechanism.

AUTHOR: Katan-Khaykovich Yael; Shaul Yosef(a)

AUTHOR ADDRESS: (a)Department of Molecular Genetics, The Weizmann Institute of Science, Rehovot, 76100: yosef.shaul@weizmann.ac.il**Israel

JOURNAL: European Journal of Biochemistry 268 (10):p3108-3116 May, 2001

MEDIUM: print

ISSN: 0014-2956

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: RFX1 binds and regulates the enhancers of a number of viruses and cellular genes. RFX1 belongs to the evolutionarily conserved RFX protein family that shares a DNA-binding domain and a conserved C-terminal region. In RFX1 this conserved region mediates dimerization, and is followed by a unique C-terminal tail, containing a highly acidic stretch. In HL-60 cells nuclear translocation of RFX1 is regulated by protein kinase C with unknown mechanisms. By confocal fluorescence microscopy, we have *identified* a nonclassical *nuclear* *localization* *signal* (NLS) at the extreme C-terminus. The adjacent 'acidic region', which showed no independent NLS activity, potentiated the function of the NLS. Subcellular fractionation showed that the tight association of RFX1 with the nucleus is mediated by its DNA-binding domain and enhanced by the dimerization domain. In contrast, the acidic region inhibited nuclear association, by down-regulating the DNA-binding activity of RFX1. These data suggest an autoinhibitory interaction, which may regulate the

function of RFX1 at the level of DNA binding. The C-terminal tail thus constitutes a composite localization domain, which on the one hand mediates nuclear import of RFX1, and on the other hand inhibits its association with the nucleus and binding to DNA. The participation of the acidic region in both activities suggests a mechanism by which the nuclear import and DNA-binding activity of RFX1 may be coordinately regulated by phosphorylation by kinases such as PKC.

REGISTRY NUMBERS: 141436-78-4: PROTEIN KINASE C

DESCRIPTORS:

MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics); Cell Biology

BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGANISMS: HL-60 cell line (Hominidae)

ORGANISMS: PARTS ETC: nucleus

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Chordates; Humans; Mammals; Primates; Vertebrates

CHEMICALS & BIOCHEMICALS: DNA; RFX1; protein kinase C

METHODS & EQUIPMENT: confocal fluorescence microscopy--analytical method

MISCELLANEOUS TERMS: protein-DNA interaction

CONCEPT CODES:

02502 Cytology and Cytochemistry-General

02508 Cytology and Cytochemistry-Human

03502 Genetics and Cytogenetics-General

03508 Genetics and Cytogenetics-Human

10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines

10802 Enzymes-General and Comparative Studies; Coenzymes

BIOSYSTEMATIC CODES:

86215 Hominidae

6/9/4 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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13116965 BIOSIS NO.: 200100324114

Nuclear localization of Schizosaccharomyces pombe Mcm2/Cdc19p requires MCM complex assembly.

AUTHOR: Pasion Sally G; Forsburg Susan L(a)

AUTHOR ADDRESS: (a)Molecular Biology and Virology Laboratory, Salk
Institute for Biological Studies, La Jolla, CA, 92037: forsburg@salk.edu
**USA

JOURNAL: Molecular Biology of the Cell 10 (12):p4043-4057 December, 1999

MEDIUM: print

ISSN: 1059-1524

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: The minichromosome maintenance (MCM) proteins MCM2-MCM7 are conserved eukaryotic replication factors that assemble in a heterohexameric complex. In fission yeast, these proteins are nuclear throughout the cell cycle. In studying the mechanism that regulates assembly of the MCM complex, we analyzed the cis and trans elements required for nuclear localization of a single subunit, Mcm2p. Mutation of any single mcm gene leads to redistribution of wild-type MCM subunits to the cytoplasm, and this redistribution depends on an active nuclear export system. We *identified* the *nuclear* *localization* *signal* sequences of Mcm2p and showed that these are required for nuclear targeting of other MCM subunits. In turn, Mcm2p must associate with other MCM proteins for its proper localization; nuclear localization of MCM proteins thus requires assembly of MCM proteins in a complex. We suggest that coupling complex assembly to nuclear targeting and retention ensures that only intact heterohexameric MCM complexes remain nuclear.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology

BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae

ORGANISMS: Schizosaccharomyces pombe (Ascomycetes)

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Fungi; Microorganisms;
Nonvascular Plants; Plants
CHEMICALS & BIOCHEMICALS: MCM2-Cdc19p--minichromosome maintenance
proteins, nuclear localization; MCM2-MCM7--minichromosome maintenance
proteins; minichromosome maintenance proteins {MCM}
MISCELLANEOUS TERMS: cell cycle
CONCEPT CODES:
10060 Biochemical Studies-General
02502 Cytology and Cytochemistry-General
02504 Cytology and Cytochemistry-Plant
51522 Plant Physiology, Biochemistry and Biophysics-Chemical
Constituents
BIOSYSTEMATIC CODES:
15100 Ascomycetes

6/9/5 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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13019003 BIOSIS NO.: 200100226152
Identification and characterization of a Drosophila nuclear proteasome
regulator: A homolog of human 11 S REGgamma (PA28gamma).
AUTHOR: Masson Patrick; Andersson Oskar; Petersen Ulla-Maja; Young Patrick
(a)
AUTHOR ADDRESS: (a)Department of Molecular Biology, Stockholm University,
S-10691, Stockholm: patrick.young@molbio.su.se**Sweden
JOURNAL: Journal of Biological Chemistry 276 (2):p1383-1390 January 12,
2001
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: We report the cloning and characterization of a Drosophila
proteasome 11 S REGgamma (PA28) homolog. The 28-kDa protein shows 47%
identity to the human REGgamma and strongly enhances the trypsin-like
activities of both Drosophila and mammalian 20 S proteasomes.
Surprisingly, the Drosophila REG was found to inhibit the proteasome's
chymotrypsin-like activity against the fluorogenic peptide
succinyl-LLVY-7-amino-4-methylcoumarin. Immunocytological analysis
reveals that the Drosophila REG is localized to the nucleus but is
distributed throughout the cell when nuclear envelope breakdown occurs
during mitosis. Through site-directed mutagenesis studies, we have
identified a functional *nuclear* *localization* *signal* present in
the homolog-specific insert region. The Drosophila PA28 NLS is similar to
the oncogene c-Myc nuclear localization motif. Comparison between
uninduced and innate immune induced Drosophila cells suggests that the
REGgamma proteasome activator has a role independent of the invertebrate
immune system. Our results support the idea that gamma class proteasome
activators have an ancient conserved function within metazoans and were
present prior to the emergence of the alpha and beta REG classes.

REGISTRY NUMBERS: 140879-24-9: PROTEASOME

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Methods and
Techniques
BIOSYSTEMATIC NAMES: Diptera--Insecta, Arthropoda, Invertebrata, Animalia
ORGANISMS: Drosophila melanogaster (Diptera)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Arthropods; Insects;
Invertebrates
CHEMICALS & BIOCHEMICALS: dREG-gamma--characterization, identification,
nuclear proteasome regulator; proteasome--chymotrypsin-like activity,
trypsin-like activity
METHODS & EQUIPMENT: DNA cloning--Recombinant DNA Technology, genetic
method; site-directed mutagenesis--genetic method, mutagenesis,
protein engineering
CONCEPT CODES:
10060 Biochemical Studies-General

10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
 10064 Biochemical Studies-Proteins, Peptides and Amino Acids
 10802 Enzymes-General and Comparative Studies; Coenzymes
 64076 Invertebrata, Comparative and Experimental Morphology, Physiology
 and Pathology-Insecta-Physiology

BIOSYSTEMATIC CODES:

75314 Diptera
 ?ds

Set	Items	Description
S1	9	AU="UEKI NOBUHIDE"
S2	9	RD (unique items)
S3	3	LEXA(S)NUCLEAR(W)LOCALIZATION(W)SIGNAL
S4	2	RD (unique items)
S5	124	NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?
S6	71	RD (unique items)

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	71	S6
	17783	LACZ
S7	0	S6 AND LACZ

?s s6 and reporter

	71	S6
	44730	REPORTER
S8	5	S6 AND REPORTER

?rd

...completed examining records

S9	5	RD (unique items)
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?t/9/all

9/9/1 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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12874064 BIOSIS NO.: 200100081213

A constitutive region is responsible for nuclear targeting of 4.1R:
 Modulation by alternative sequences results in differential intracellular
 localization.

AUTHOR: Luque Carlos M; Correas Isabel(a)

AUTHOR ADDRESS: (a)Centro de Biologia Molecular 'Severo Ochoa' (CSIC/UAM),
 Universidad Autonoma de Madrid, E-28049, Madrid: icorreas@cbm.uam.es**
 Spain

JOURNAL: Journal of Cell Science 113 (13):p2485-2495 July, 2000

MEDIUM: print

ISSN: 0021-9533

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: Red blood cell protein 4.1, 4.1R, is an extreme variation on the theme of isoform multiplicity. The diverse 4.1R isoforms, mainly generated by alternative pre-mRNA splicing, are localized at different intracellular sites, including the nucleus. To characterize nonerythroid 4.1 proteins lacking the most upstream translation initiation site, analyze their intracellular localization and define specific domains involved in differential intracellular targeting of 4.1R, we cloned 4.1 cDNAs lacking that translation initiation site. Seven different 4.1R cDNAs were isolated. Four of these encoded 4.1R proteins localized predominantly to the nucleus and the other three localized to the cytoplasm. Three of the nuclear 4.1R isoforms did not contain the *nuclear* *localization* *signal* previously *identified* in the alternative exon 16. A comparative analysis of the exon composition of the naturally occurring 4.1R cDNAs cloned and of appropriate composite cDNA constructs, with the subcellular distribution of their respective products, demonstrated that a region encoded by constitutive exons, which is therefore common to all 4.1R isoforms and has been termed 'core region', had the capacity of localizing to the nucleus. This region was able to confer nuclear targeting to a cytosolic *reporter*. In protein 4.1R isoforms, the nuclear targeting of the core region is modulated by the expression of alternative exons. Thus, exon 5-encoded sequences eclipsed nuclear entry of the core region, resulting in 4.1R isoforms

that predominantly distributed to the cytoplasm. Exon 5 was also able to confer cytoplasmic localization to a nuclear *reporter*. In protein 4.1R isoforms, when exons 5 and 16 were both expressed the nuclear targeting effect of exon 16 was dominant to the inhibitory effect observed by the expression of exon 5, yielding proteins that predominantly localized to the nucleus. Taken together, these results indicate that all 4.1R molecules contain a conserved region that is sufficient to target the protein to the nucleus, but that specific exon-encoded sequences modulate this capacity by acting in a hierarchical order.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology;

Blood and Lymphatics (Transport and Circulation)

BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGANISMS: MOLT-4 cell line (Hominidae)--human T lymphoid cells

ORGANISMS: PARTS ETC: red blood cell--blood and lymphatics

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Chordates; Humans;

Mammals; Primates; Vertebrates

CHEMICALS & BIOCHEMICALS: 4.1R protein--alternative sequences, constitutive region, intracellular localization, nuclear targeting, red blood cell protein

CONCEPT CODES:

02508 Cytology and Cytochemistry-Human

02502 Cytology and Cytochemistry-General

02506 Cytology and Cytochemistry-Animal

10060 Biochemical Studies-General

15002 Blood, Blood-Forming Organs and Body Fluids-Blood and Lymph Studies

15004 Blood, Blood-Forming Organs and Body Fluids-Blood Cell Studies

BIOSYSTEMATIC CODES:

86215 Hominidae

9/9/2 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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12779863 BIOSIS NO.: 200000533486

Gene activation by varicella-zoster virus IE4 protein requires its dimerization and involves both the Arginine-rich sequence, the central part, and the carboxyl-terminal cysteine-rich region.

AUTHOR: Baudoux Laurence; Defechereux Patricia; Rentier Bernard; Piette Jacques(a)

AUTHOR ADDRESS: (a)Laboratory of Fundamental Virology and Immunology, Institute of Pathology, University of Liege, B23, B-4000, Liege**Belgium

JOURNAL: Journal of Biological Chemistry 275 (42):p32822-32831 October 20, 2000

MEDIUM: print

ISSN: 0021-9258

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: Varicella-zoster virus (VZV) open reading frame 4-encoded protein (IE4) possesses transactivating properties for VZV genes as well as for those of heterologous viruses. Since most transcription factors act as dimers, IE4 dimerization was studied using the mammalian two-hybrid system. Introduction of mutations in the IE4 open reading frame demonstrated that both the central region and the carboxyl-terminal cysteine-rich domain were important for efficient dimerization. Within the carboxyl-terminal domain, substitution of amino acids encompassing residues 443-447 totally abolished dimerization. Gene activation by IE4 was studied by transient transfection with an IE4 expression plasmid and a *reporter* gene under the control of either the human immunodeficiency virus, type 1, long terminal repeat or the VZV thymidine kinase promoter. Regions of IE4 important for dimerization were also shown to be crucial for transactivation. In addition, the arginine-rich domains Rb and Rc of the amino-terminal region were also demonstrated to be important for transactivation, whereas the Ra domain as well as an acidic and

bZIP-containing regions were shown to be dispensable for gene transactivation. A nucleocytoplasmic shuttling of IE4 has also been characterized, involving a *nuclear* *localization* *signal* *identified* within the Rb domain and a nuclear export mechanism partially depending on Crm-1.

REGISTRY NUMBERS: 52-90-4Q: CYSTEINE; 3374-22-9Q: CYSTEINE; 9002-06-6: THYMIDINE KINASE

DESCRIPTORS:

MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics)

BIOSYSTEMATIC NAMES: Herpesviridae--Animal Viruses, Viruses, Microorganisms; Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae--Animal Viruses, Viruses, Microorganisms

ORGANISMS: HeLa cell line (Hominidae); human immunodeficiency virus-1 (Retroviridae); varicella-zoster virus (Herpesviridae)--pathogen

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

CHEMICALS & BIOCHEMICALS: amino acids; cysteine; plasmids; proteins; *reporter* genes; thymidine kinase--promoter; transcription factors --functions; viral IE4 proteins--analysis, dimerization, functions, molecular regions, nucleocytoplasmic shuttling, structures; viral proteins--analysis, functions

MISCELLANEOUS TERMS: gene mutations; open reading frames; protein nuclear export mechanisms--analysis; viral gene activation mechanisms --analysis; viral genetics

CONCEPT CODES:

10064 Biochemical Studies-Proteins, Peptides and Amino Acids
02508 Cytology and Cytochemistry-Human
03502 Genetics and Cytogenetics-General
03508 Genetics and Cytogenetics-Human
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10802 Enzymes-General and Comparative Studies; Coenzymes
31500 Genetics of Bacteria and Viruses
33506 Virology-Animal Host Viruses

BIOSYSTEMATIC CODES:

02612 Herpesviridae (1993-)
02623 Retroviridae (1993-)
86215 Hominidae

9/9/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09975122 BIOSIS NO.: 199598430040

A polymorphic bipartite motif signals nuclear targeting of early auxin-inducible proteins related to PS-IAA4 from pea (*Pisum sativum*).

AUTHOR: Abel Steffen; Theologis Athanasios(a)

AUTHOR ADDRESS: (a)Plant Gene Expression Cent., 800 Buchanan Street, Albany, CA 94710*USA

JOURNAL: Plant Journal 8 (1):p87-96 1995

ISSN: 0960-7412

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The plant hormone, indoleacetic acid (IAA), transcriptionally activates two early genes in pea, PS-IAA4/5 and PS-IAA6, that encode short-lived nuclear proteins. The identification of the nuclear localization signals (NLS) in PS-IAA4 and PS-IAA6 using progressive deletion analysis and site-directed mutagenesis is reported. A C-terminal SV40-type NLS is sufficient to direct the beta-glucuronidase *reporter* to the nucleus of transiently transformed tobacco protoplasts, but is dispensable for nuclear localization of both proteins. The dominant and essential NLS in PS-IAA4 and PS-IAA6 overlap with a bipartite basic motif which is polymorphic and conserved in related proteins from other plant species, having the consensus sequence (KKNEK)KR-X-(24-71)-(RSXRK)/(RK/RK). Both basic elements of this motif in PS-IAA4, (KR-X-41-RSYRK), function interdependently as a bipartite NLS.

However, in PS-IAA6 (KKNEKKR-X-36-RKK) the upstream element of the corresponding motif contains additional basic residues which allow its autonomous function as an SV40-type monopartite NLS. The spacer-length polymorphism, X-(24-70), in respective bipartite NLS peptides of several PS-IAA4-like proteins from *Arabidopsis thaliana* does not affect nuclear targeting function. The structural and functional variation of the bipartite basic motif in PS-IAA4-like proteins supports the proposed integrated consensus of NLS.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology;
Chemical Coordination and Homeostasis; Genetics; Physiology
BIOSYSTEMATIC NAMES: Leguminosae--Dicotyledones, Angiospermae,
Spermatophyta, Plantae
ORGANISMS: *Pisum sativum* (Leguminosae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): angiosperms; dicots; plants;
spermatophytes; vascular plants
MISCELLANEOUS TERMS: FUNCTIONAL VARIATION; GENETIC TRANSFORMATION;
NUCLEAR *LOCALIZATION* *SIGNAL* *IDENTIFICATION*; PHYTOHORMONE;
PROGRESSIVE DELETION ANALYSIS; PS-IAA4-LIKE PROTEINS; SITE-DIRECTED
MUTAGENESIS; STRUCTURAL VARIATION

CONCEPT CODES:

02504 Cytology and Cytochemistry-Plant
03504 Genetics and Cytogenetics-Plant
10060 Biochemical Studies-General
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
51514 Plant Physiology, Biochemistry and Biophysics-Growth Substances
51520 Plant Physiology, Biochemistry and Biophysics-Translocation,
Accumulation
51522 Plant Physiology, Biochemistry and Biophysics-Chemical
Constituents

BIOSYSTEMATIC CODES:

26260 Leguminosae

9/9/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09765420 BIOSIS NO.: 199598220338

Nucleo-cytoplasmic distribution of human hnRNP proteins: A search for the targeting domains in hnRNP A1.

AUTHOR: Weighardt Florian(a); Biamonti Giuseppe; Riva Silvano

AUTHOR ADDRESS: (a)Ist. Genetica Biochimica Evoluzionistica del, CNR, Univ.
degli Studi di Pavia, Via Abbiategrasso **Italy

JOURNAL: Journal of Cell Science 108 (2):p545-555 1995

ISSN: 0021-9533

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: hnRNP A1 (34 kDa) is an RNA binding protein consisting of two tandemly arranged RNA binding domains C-terminally linked to a glycine-rich auxiliary domain (2 times RBDGly). A1 belongs to the set of polypeptides that bind nascent hnRNA in the nucleus to form the so called hnRNP complexes. These complexes seem to be involved both in pre-mRNA processing and in the nuclear export of mRNA. In fact A1, along with other hnRNP proteins, is exported from the nucleus probably bound to mRNA and is immediately re-imported. A1 nuclear re-import, which requires active transcription, is not mediated by a canonical *nuclear* *localization* *signal* (NLS). To *identify* the determinants of A1 subcellular localization we developed an expression vector for studying the localization. in transiently transfected cells, of the different structural motifs of A1 fused to a small *reporter* protein (chloramphenicol acetyltransferase, CAT; 26 kDa). We demonstrate that a 30 amino acid sequence in the glycine-rich domain (YNDFGNYNQSSNFGPMKGGNFGGRSSGPY), which bears no resemblance to canonical NLS, is necessary and sufficient to target the protein to the nucleus. Our data suggest that this targeting sequence might act by mediating the interaction of A1 with a NLS-containing nuclear import complex. On the

other hand, the nuclear export of A1 requires at least one RNA binding domain in accord with the hypothesis that A1 exits from the nucleus bound to mRNA. We propose a mechanism for the nucleo-cytoplasmic shuttling of A1 that envisages a specific role for the different structural domains and can explain the dependence of nuclear import from active transcription.

REGISTRY NUMBERS: 9040-07-7: CHLORAMPHENICOL ACETYLTRANSFERASE

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Molecular Genetics (Biochemistry and Molecular Biophysics); Morphology; Physiology

BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGANISMS: Hominidae (Hominidae)

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; humans; mammals; primates; vertebrates

CHEMICALS & BIOCHEMICALS: CHLORAMPHENICOL ACETYLTRANSFERASE

MOLECULAR SEQUENCE DATABANK NUMBER: molecular sequence data; nucleotide sequence

MISCELLANEOUS TERMS: CHLORAMPHENICOL ACETYLTRANSFERASE; HETEROGENEOUS NUCLEAR RNA; MESSENGER RNA; SHUTTLE MECHANISM; TRANSCRIPTION

CONCEPT CODES:

02508 Cytology and Cytochemistry-Human
03508 Genetics and Cytogenetics-Human
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10300 Replication, Transcription, Translation
10506 Biophysics-Molecular Properties and Macromolecules
10806 Enzymes-Chemical and Physical
11108 Anatomy and Histology, General and Comparative-Microscopic and Ultramicroscopic Anatomy
12100 Movement (1971-)
13012 Metabolism-Proteins, Peptides and Amino Acids
13014 Metabolism-Nucleic Acids, Purines and Pyrimidines
10052 Biochemical Methods-Nucleic Acids, Purines and Pyrimidines
10054 Biochemical Methods-Proteins, Peptides and Amino Acids

BIOSYSTEMATIC CODES:

86215 Hominidae

9/9/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08931054 BIOSIS NO.: 199396082555

The matrix protein of Newcastle disease virus localizes to the nucleus via a bipartite nuclear localization signal.

AUTHOR: Coleman Natalie A; Peeples Mark E(a)

AUTHOR ADDRESS: (a)Dep. Immunol./Microbiol., St. Luke's Med. Cent., 1653 West Congress Parkway, Chicago, IL 60612**USA

JOURNAL: Virology 195 (2):p596-607 1993

ISSN: 0042-6822

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The Newcastle disease virus matrix (M) protein expressed from a cDNA clone is observed in the nucleus of transfected cells, displaying a localization pattern identical to that observed in virus-infected cells. To *identify* the *nuclear* *localization* *signal* (NLS) in the M protein, M gene mutants encoding deletion and amino acid substitution proteins were constructed and expressed transiently in COS-1 cells. Protein products were examined for intracellular localization using indirect immunofluorescence. Two basic amino acid clusters in the M protein were found to be required for nuclear localization since deletion of these basic clusters or substitution with random amino acids resulted in cytoplasmic localization. Substitution of pairs of basic amino acids with non-basic residues revealed that components from both basic regions are required for nuclear localization. This interdependence between two

basic clusters suggests that the NLS in the M protein belongs to the newly described class of "bipartite" NLSs. Unlike most NLSs, M protein sequences containing the critical basic amino acid clusters fused to two different cytoplasmic *reporter* proteins failed to transport these proteins to the nucleus.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Microbiology

BIOSYSTEMATIC NAMES: Cercopithecidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Paramyxoviridae--Viruses; Retroviridae--Viruses

ORGANISMS: simian immunodeficiency virus (Retroviridae); Cercopithecidae (Cercopithecidae); Paramyxoviridae (Paramyxoviridae)

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; mammals; microorganisms; nonhuman mammals; nonhuman primates; nonhuman vertebrates; primates; vertebrates; viruses

MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; molecular sequence data

MISCELLANEOUS TERMS: CELL TROPISM; ENV GENE; LYMPHOCYTE; MACROPHAGE

CONCEPT CODES:

02506 Cytology and Cytochemistry-Animal
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
33506 Virology-Animal Host Viruses
31500 Genetics of Bacteria and Viruses

BIOSYSTEMATIC CODES:

02617 Paramyxoviridae (1993-)
86205 Cercopithecidae

?ds

Set	Items	Description
S1	9	AU="UEKI NOBUHIDE"
S2	9	RD (unique items)
S3	3	LEXA(S)NUCLEAR(W)LOCALIZATION(W)SIGNAL
S4	2	RD (unique items)
S5	124	NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?
S6	71	RD (unique items)
S7	0	S6 AND LACZ
S8	5	S6 AND REPORTER
S9	5	RD (unique items)

?s nuclear(w)localization(w)signal(2n)assay

438217 NUCLEAR
297004 LOCALIZATION
4 SIGNAL
580197 ASSAY

S10 0 NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)ASSAY

?s nuclear(w)localization(w)signal(s)assay

438217 NUCLEAR
297004 LOCALIZATION
343956 SIGNAL
580197 ASSAY

S11 200 NUCLEAR(W)LOCALIZATION(W)SIGNAL(S)ASSAY

?s s11 and lacz

200 S11
17783 LACZ

S12 4 S11 AND LACZ

?rd

...completed examining records

S13 2 RD (unique items)

?t/9/all

13/9/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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12821664 BIOSIS NO.: 200100028813

Evaluation of a new tool for exploring podocyte biology: Mouse Nphs1 5' flanking region drives *lacZ* expression in podocytes.

AUTHOR: Moeller Marcus J; Kovari Iulia A; Holzman Lawrence B(a)

AUTHOR ADDRESS: (a)University of Michigan Medical School, 1560 Medical Science Research Building II, Ann Arbor, MI, 48109-0676:

lholzman@umich.edu**USA
JOURNAL: Journal of the American Society of Nephrology 11 (12):p2306-2314
December, 2000
MEDIUM: print
ISSN: 1046-6673
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Study of podocyte biology has been hampered by limitations in available experimental models that both recapitulate the in vivo phenotypes of this cell and can be readily and specifically manipulated at the molecular level. Transgenic manipulation of the podocyte represents one approach that might circumvent these limitations. The purpose of this study was to identify a promoter-enhancer that would direct the expression of transgenes in a podocyte-specific manner. The nephrin (Nphs1) promoter was considered a good candidate for this purpose, because nephrin was thought to be expressed exclusively in podocytes. Two independent BAC clones that contained the murine Nphs1 gene were identified. An 8.3-kb and a 5.4-kb fragment containing the 5' flanking promoter sequence were identified and characterized. Two constructs were generated by placing a bacterial *lacZ* reporter with a *nuclear* *localization* *signal* under the control of these two DNA fragments. Mice transgenic for both constructs were generated. Using a chemiluminescence *assay*, beta-galactosidase activity significantly above control was detected only in tissue homogenates of kidneys and brain of transgenic mice. In X-gal stained sections of transgenic adult kidneys, only podocyte nuclei expressed beta-galactosidase. In adult brain examined by tissue sectioning, beta-galactosidase activity was confined to a discrete area in the medulla. Identical patterns of beta-galactosidase expression were observed in multiple transgenic founders, suggesting that the expression pattern observed was independent of the site of transgene integration. The developmental expression of beta-galactosidase in transgenic embryos was also analyzed. Transgenes regulated by this promoter should be useful for studying the biology of gene products that regulate podocyte phenotype and function.

REGISTRY NUMBERS: 9031-11-2: BETA-GALACTOSIDASE; 65136-96-1: NEPHRIN
DESCRIPTORS:

MAJOR CONCEPTS: Urinary System (Chemical Coordination and Homeostasis)
BIOSYSTEMATIC NAMES: Muridae--Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: mouse (Muridae)
ORGANISMS: PARTS ETC: podocyte--excretory system; renal medulla--excretory system
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
CHEMICALS & BIOCHEMICALS: *LacZ*--expression; X-gal; beta-galactosidase; nephrin; nephrin promoter
GENE NAME: Nphs1 gene (Muridae)--flanking region
METHODS & EQUIPMENT: chemiluminescence assay--analytical method, detection/labeling techniques

CONCEPT CODES:

15504 Urinary System and External Secretions-Physiology and Biochemistry
02506 Cytology and Cytochemistry-Animal
03506 Genetics and Cytogenetics-Animal
10802 Enzymes-General and Comparative Studies; Coenzymes

BIOSYSTEMATIC CODES:

86375 Muridae

13/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09666463 BIOSIS NO.: 199598121381

Human foamy virus Bell transactivator contains a bipartite nuclear localization determinant which is sensitive to protein context and triple multimerization domains.

AUTHOR: Chang Jun; Lee Ki Jeong; Jang Kyung Lib; Lee Eun Kyeong; Baek Gwan Hyuk; Sung Young Chul(a)
 AUTHOR ADDRESS: (a)Dep. Life Sci., Pohang Univ. Sci. Technol., Pohang 790-784**North Korea
 JOURNAL: Journal of Virology 69 (2):p801-808 1995
 ISSN: 0022-538X
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: The Bell protein of human foamy virus is a 300-amino-acid nuclear regulatory protein which transactivates the gene expression directed by the homologous long terminal repeat and the human immunodeficiency virus type I long terminal repeat. While previous reports suggested that the single basic domain of Bell from residues 211 to 222 and/or 209 to 226 is necessary and sufficient for efficient nuclear localization (L. K. Venkatesh, C. Yang, P. A. Theodorakis, and G. Chinnandurai, J. Virol. 67:161-169, 1993; F. He, J. D. Sun, E. D. Garrett, and B. R. Cullen, J. Virol. 67:1896-1904, 1993), our recent data showed that another basic domain, from amino acid residues 199 to 200, is also required for nuclear localization of Bell (C. W. Lee, C. Jun, K. J. Lee, and Y. C. Sung, J. Virol. 68:2708-2719, 1994). To clarify this discrepancy, we constructed various bell-*lacZ* chimeric constructs and several linker insertion mutants and determined their subcellular localization. When the region of Bell containing basic domains was placed at an internal site of the *lacZ* gene, the *nuclear* *localization* *signal* (NLS) of Bell consisted of two discontinuous basic regions separated by an intervening sequence. Moreover, insertion of specific amino acids between two basic regions disrupted the activity of the Bell NLS. On the other hand, Bell residues 199 and 200 were not required to direct the Bell-beta-galactosidase chimeric protein to the nucleus when the Bell NLS was appended to the amino terminus of beta-galactosidase. These results indicate that the function of the Bell NLS is sensitive to the protein context within which the sequence is present. In addition, we demonstrated that the Bell protein forms a multimeric complex in the nuclei of mammalian cells by using a sensitive in vivo protein-protein interaction *assay*. Mutational analyses revealed that the regions which mediate multimer formation map to three domains of Bell, i.e., residues 1 to 31, 42 to 82, and 82 to 111. Furthermore, our results show that the region of Bell from residues 202 to 226 prevents Bell from forming a multimeric complex.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Microbiology; Molecular Genetics (Biochemistry and Molecular Biophysics)

BIOSYSTEMATIC NAMES: Mammalia-Unspecified--Mammalia, Vertebrata, Chordata, Animalia; Retroviridae--Viruses

ORGANISMS: Mammalia (Mammalia - Unspecified); Retroviridae (Retroviridae)

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; mammals; microorganisms; nonhuman mammals; nonhuman vertebrates; vertebrates; viruses

MISCELLANEOUS TERMS: MAMMALIAN CELLS; TRANSCRIPTIONAL GENE REGULATION

CONCEPT CODES:

10064 Biochemical Studies-Proteins, Peptides and Amino Acids
 10300 Replication, Transcription, Translation
 10506 Biophysics-Molecular Properties and Macromolecules
 31500 Genetics of Bacteria and Viruses
 33506 Virology-Animal Host Viruses
 02506 Cytology and Cytochemistry-Animal

BIOSYSTEMATIC CODES:

02623 Retroviridae (1993-)
 85700 Mammalia-Unspecified

?ds

Set	Items	Description
S1	9	AU="UEKI NOBUHIDE"
S2	9	RD (unique items)
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S4	2	RD (unique items)
S5	124	NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?

S6 71 RD (unique items)
 S7 0 S6 AND LACZ
 S8 5 S6 AND REPORTER
 S9 5 RD (unique items)
 S10 0 NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)ASSAY
 S11 200 NUCLEAR(W)LOCALIZATION(W)SIGNAL(S)ASSAY
 S12 4 S11 AND LACZ
 S13 2 RD (unique items)

?s s11 and reporter

200 S11
 44730 REPORTER
 S14 21 S11 AND REPORTER

?rd

...completed examining records
 S15 12 RD (unique items)

?s s15 and fusion

12 S15
 175110 FUSION
 S16 3 S15 AND FUSION

?rd

...completed examining records
 S17 3 RD (unique items)

?t/9/all

17/9/1 (Item 1 from file: 5)
 DIALOG(R)File 5: Biosis Previews(R)
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11469998 BIOSIS NO.: 199800251330

Intrinsic transcriptional activation-inhibition domains of the polyomavirus enhancer binding protein 2/core binding factor alpha subunit revealed in the presence of the beta subunit.

AUTHOR: Kanno Tomohiko; Kanno Yuka; Chen Lin-Feng; Ogawa Eiko; Kim Woo-Young; Ito Yoshiaki(a)

AUTHOR ADDRESS: (a)Inst. Virus Res., Kyoto Univ., Shogo-ku, Kyoto 606** Japan

JOURNAL: Molecular and Cellular Biology 18 (5):p2444-2454 May, 1998

ISSN: 0270-7306

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: A member of the polyomavirus enhancer binding protein 2/core binding factor (PEBP2/CBF) is composed of PEBP2alphaB1/AML1 (as the alpha subunit) and a beta subunit. It plays an essential role in definitive hematopoiesis and is frequently involved in the chromosomal abnormalities associated with leukemia. In the present study, we report functionally separable modular structures in PEBP2alphaB1 for DNA binding and for transcriptional activation. DNA binding through the Runt domain of PEBP2alphaB1 was hindered by the adjacent carboxy-terminal region, and this inhibition was relieved by interaction with the P subunit. Utilizing a *reporter* *assay* system in which both the alpha and beta subunits are required to achieve strong transactivation, we uncovered the presence of transcriptional activation and inhibitory domains in PEBP2alphaB1 that were only apparent in the presence of the beta subunit. The inhibitory domain keeps the full transactivation potential of full-length PEBP2alphaB1 below its maximum potential. *Fusion* of the transactivation domain of PEBP2alphaB1 to the yeast GAL4 DNA-binding domain conferred transactivation potential, but further addition of the inhibitory domain diminished the activity. These results suggest that the activity of the alpha subunit as a transcriptional activator is regulated intramolecularly as well as by the beta subunit. PEBP2alphaB1 and the beta subunit were targeted to the nuclear matrix via signals distinct from the *nuclear* *localization* *signal*. Moreover, the transactivation domain by itself was capable of associating with the nuclear matrix, which implies the existence of a relationship between transactivation and nuclear matrix attachment.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics

CHEMICALS & BIOCHEMICALS: polyomavirus enhancer binding protein 2/core

binding factor {PEBP2/CBF}--alpha subunit, beta subunit, transcription
factor, transcriptional activation-inhibition domains
CONCEPT CODES:
10060 Biochemical Studies-General
03502 Genetics and Cytogenetics-General

17/9/2 (Item 2 from file: 5)
DIALOG(R)File 5: Biosis Previews(R)
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10609221 BIOSIS NO.: 199699230366
Analysis of the VPg-proteinase (NIa) encoded by tobacco etch potyvirus:
Effects of mutations on subcellular transport, proteolytic processing,
and genome amplification.
AUTHOR: Schaad Mary C; Haldeman-Cahil Ruth; Cronin Stephen; Carrington
James C(a)
AUTHOR ADDRESS: (a)Dep. Biol., Texas A and M Univ., College Station, TX
77843**USA
JOURNAL: Journal of Virology 70 (10):p7039-7048 1996
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A mutational analysis was conducted to investigate the functions
of the tobacco etch potyvirus VPg-proteinase (NIa) protein in vivo. The
NIa N-terminal domain contains the VPg attachment site, whereas the
C-terminal domain contains a picornavirus 3C-like proteinase. Cleavage at
an internal site separating the two domains occurs in a subset of NIa
molecules. The majority of NIa molecules in TEV-infected cells accumulate
within the nucleus. By using a *reporter* *fusion* strategy, the NIa
nuclear *localization* *signal* was mapped to a sequence within amino
acid residues 40 to 49 in the VPg domain. Mutations resulting in
debilitation of NIa nuclear translocation also debilitated genome
amplification, suggesting that the NLS overlaps a region critical for RNA
replication. The internal cleavage site was shown to be a poor substrate
for NIa proteolysis because of a suboptimal sequence context around the
scissile bond. Mutants that encoded NIa variants with accelerated
internal proteolysis exhibited genome amplification defects, supporting
the hypothesis that slow internal processing provides a regulatory
function. Mutations affecting the VPg attachment site and proteinase
activesite residues resulted in amplification-defective viruses. A
transgenic complementation *assay* was used to test whether NIa supplied
in trans could rescue amplification-defective viral genomes encoding
altered NIa proteins. Neither cells expressing NIa alone nor cells
expressing a series of NIa-containing polyproteins supported increased
levels of amplification of the mutants. The lack of complementation of
NIa-defective mutants is in contrast to previous results obtained with
RNA polymerase (NIb)-defective mutants, which were relatively efficiently
rescued in the transgenic complementation *assay*. It is suggested that,
unlike NIb polymerase, NIa provides replicative functions that are cis
preferential.

REGISTRY NUMBERS: 154907-71-8: VPG-PROTEINASE

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Enzymology
(Biochemistry and Molecular Biophysics); Genetics; Microbiology;
Molecular Genetics (Biochemistry and Molecular Biophysics)

BIOSYSTEMATIC NAMES: Potyvirus--Viruses; Solanaceae--Dicotyledones,
Angiospermae, Spermatophyta, Plantae

ORGANISMS: tobacco etch potyvirus (Potyvirus); Nicotiana tabacum
(Solanaceae)

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): angiosperms; dicots;
microorganisms; plants; spermatophytes; vascular plants; viruses

CHEMICALS & BIOCHEMICALS: VPG-PROTEINASE

MISCELLANEOUS TERMS: CULTIVAR-XANTHI; ENZYMOLOGY; GENOME AMPLIFICATION;

MOLECULAR GENETICS; PROTEOLYTIC PROCESSING; RNA REPLICATION;

SUBCELLULAR TRANSPORT; VPG-PROTEINASE

CONCEPT CODES:

10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids

10300 Replication, Transcription, Translation
 10506 Biophysics-Molecular Properties and Macromolecules
 10806 Enzymes-Chemical and Physical
 31500 Genetics of Bacteria and Viruses
 33508 Virology-Plant Host Viruses
 BIOSYSTEMATIC CODES:
 02829 Potyvirus (1993-)
 26775 Solanaceae

17/9/3 (Item 1 from file: 155)
 DIALOG(R)File 155:MEDLINE(R)

11444021 21282977 PMID: 11279056
 Starvation promotes nuclear accumulation of the hsp70 Ssa4p in yeast cells.
 Chughtai ZS; Rassadi R; Matusiewicz N; Stochaj U
 Department of Physiology, McGill University, Montreal, Province of Quebec
 H3G 1Y6, Canada.
 Journal of biological chemistry (United States) Jun 8 2001, 276 (23)
 p20261-6, ISSN 0021-9258 Journal Code: HIV
 Languages: ENGLISH
 Document type: Journal Article
 Record type: Completed
 Subfile: INDEX MEDICUS

Nuclear import of proteins that are too large to passively enter the nucleus requires soluble factors, energy, and a *nuclear* *localization* *signal* (NLS). Nuclear protein transport can be regulated, and different forms of stress affect nucleocytoplasmic trafficking. As such, import of proteins containing a classical NLS is inhibited in starving yeast cells. In contrast, the hsp70 Ssa4p concentrates in nuclei upon starvation. Nuclear concentration of Ssa4p in starving cells is reversible, and transfer of stationary phase cells to fresh medium induces Ssa4p nuclear export. This export reaction represents an active process that is sensitive to oxidative stress. In starving cells, the N-terminal domain of Ssa4p mediates Ssa4p nuclear accumulation, and a short hydrophobic sequence, termed Star (for starvation), is sufficient to localize the *reporter* proteins green fluorescent protein or beta-galactosidase to nuclei. To determine whether nuclear accumulation of Star-beta-galactosidase depends on a specific nuclear carrier, we have analyzed its distribution in mutant yeast strains that carry a deletion of a single beta-importin gene. With this *assay* we have identified Nmd5p as a beta-importin required to concentrate Star-beta-galactosidase in nuclei when cells enter stationary phase.

Tags: Support, Non-U.S. Gov't
 Descriptors: Cell Nucleus--metabolism--ME; *Heat-Shock Proteins 70
 --metabolism--ME; *Recombinant *Fusion* Proteins--metabolism--ME;
 *Saccharomyces cerevisiae--metabolism--ME; *Starvation; Luminescent
 Proteins--metabolism--ME; Nuclear Localization Signal; Protein Transport
 CAS Registry No.: 0 (Heat-Shock Proteins 70); 0 (Luminescent Proteins)
 ; 0 (Nuclear Localization Signal); 0 (Recombinant Fusion Proteins);
 147336-22-9 (green fluorescent protein)
 Record Date Created: 20010604
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S4	2	RD (unique items)
S5	124	NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?
S6	71	RD (unique items)
S7	0	S6 AND LACZ
S8	5	S6 AND REPORTER
S9	5	RD (unique items)
S10	0	NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)ASSAY
S11	200	NUCLEAR(W)LOCALIZATION(W)SIGNAL(S)ASSAY
S12	4	S11 AND LACZ
S13	2	RD (unique items)
S14	21	S11 AND REPORTER
S15	12	RD (unique items)

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S16          3    S15 AND FUSION
S17          3    RD (unique items)
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      297004    LOCALIZATION
      343956    SIGNAL
      46337     SCREEN
      S18       0    NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)SCREEN
?s nuclear(w)localization(w)signal(3n)detec?
      438217    NUCLEAR
      297004    LOCALIZATION
      343956    SIGNAL
      1566330   DETEC?
      S19       8    NUCLEAR(W)LOCALIZATION(W)SIGNAL(3N)DETEC?
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...completed examining records
      S20       5    RD (unique items)
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      5         S20
      44730     REPORTER
      17783     LACZ
      S21       2    S20 AND (REPORTER OR LACZ)
?rd
...completed examining records
      S22       2    RD (unique items)
?t/9/all

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22/9/1 (Item 1 from file: 5)
 DIALOG(R)File 5: Biosis Previews(R)
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12560938 BIOSIS NO.: 200000314440
 Identification of a novel signal sequence that targets transmembrane proteins to the nuclear envelope inner membrane.
 AUTHOR: Meyer Grit Angel; Radsak Klaus Dietrich
 AUTHOR ADDRESS: (a)Institut fuer Virologie der Philipps-Universitaet, Robert-Koch-Strasse 17, 35037, Marburg**Germany
 JOURNAL: Journal of Biological Chemistry 275 (6):p3857-3866 February 11, 2000
 MEDIUM: print
 ISSN: 0021-9258
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English
 SUMMARY LANGUAGE: English

ABSTRACT: Herpesvirus maturation requires translocation of glycoprotein B homologue from the endoplasmic reticulum to the inner nuclear membrane. Glycoprotein B of human cytomegalovirus was used in this context as a model protein. To identify a specific signal sequence within human cytomegalovirus glycoprotein B acting in a modular fashion, coding sequences were recombined with *reporter* proteins. Immunofluorescence and cell fractionation demonstrated that a short sequence element within the cytoplasmic tail of human cytomegalovirus glycoprotein B was sufficient to translocate the membrane protein CD8 to the inner nuclear membrane. This carboxyl-terminal sequence had no *detectable* *nuclear* *localization* *signal* activity for soluble beta-Galactosidase and could not be substituted by the nuclear localization signal of SV40 T antigen. For glycoprotein B of herpes simplex virus, a carboxyl-terminal element with comparable properties was found. Further experiments showed that the amino acid sequence DRLRHR of human cytomegalovirus glycoprotein B (amino acids 885-890) was sufficient for nuclear envelope translocation. Single residue mutations revealed that the arginine residues in positions 4 and 6 of the DRLRHR sequence were essential for its function. These results support the view that transmembrane protein transport to the inner nuclear membrane is controlled by a mechanism different from that of soluble proteins.

DESCRIPTORS:

MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics); Membranes (Cell Biology); Methods and Techniques

BIOSYSTEMATIC NAMES: Cercopithecidae--Primates, Mammalia, Vertebrata,
 Chordata, Animalia; Herpesviridae--Animal Viruses, Viruses,
 Microorganisms
 ORGANISMS: COS7 cell line (Cercopithecidae)--African green monkey kidney
 cells, transfected; cytomegalovirus (Herpesviridae); herpes simplex
 virus (Herpesviridae)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animal Viruses; Animals;
 Chordates; Mammals; Microorganisms; Nonhuman Mammals; Nonhuman Primates
 ; Nonhuman Vertebrates; Primates; Vertebrates; Viruses
 CHEMICALS & BIOCHEMICALS: glycoprotein B--amino acid sequence, analysis
 , inner nuclear membrane transport, novel signal sequence,
 transmembrane protein
 METHODS & EQUIPMENT: cell fractionation--Histological/Cytological and
 Culture Techniques, cytological method; immunofluorescence--Spectrum
 Analysis Techniques, detection method
 CONCEPT CODES:
 03502 Genetics and Cytogenetics-General
 02502 Cytology and Cytochemistry-General
 10050 Biochemical Methods-General
 10060 Biochemical Studies-General
 10502 Biophysics-General Biophysical Studies
 33502 Virology-General; Methods
 BIOSYSTEMATIC CODES:
 02612 Herpesviridae (1993-)
 86205 Cercopithecidae

22/9/2 (Item 2 from file: 5)
 DIALOG(R)File 5: Biosis Previews(R)
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10385719 BIOSIS NO.: 199699006864
 A nuclear GFP/beta-galactosidase fusion protein as a marker for
 morphogenesis in living Drosophila.
 AUTHOR: Shiga Yasuhiro; Tanaka-Matakatsu Miho; Hayashi Shigeo(a)
 AUTHOR ADDRESS: (a)Genet. Stock Res. Cent., Natl. Inst. Genet., Mishima,
 Shizuoka-ken 411**Japan
 JOURNAL: Development Growth & Differentiation 38 (1):p99-106 1996
 ISSN: 0012-1592
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: A general, non-invasive method to trace morphogenesis in living
 Drosophila was developed. To label specific cells. green fluorescence
 protein (GFP) of jellyfish Aequorea victoria was expressed by the
 Gal4-UAS system. Green fluorescence from GFP fused to the "nuclear"
 "localization" "signal" was "detectable" in polytene larval tissue, but
 not in diploid tissue. Further fusion to bacterial beta-galactosidase
 produced GFPN-*lacZ*, which fluoresced brightly in several diploid larval
 and embryonic tissues. GFPN-*lacZ* was used to trace dynamic cell
 movement during the formation of the embryonic tracheal system. These
 results indicate that GFPN-*lacZ* can be used to mark specific cells to
 study cell movement and gene expression in living animals.

REGISTRY NUMBERS: 9031-11-2: BETA-GALACTOSIDASE

DESCRIPTORS:

MAJOR CONCEPTS: Development; Genetics; Molecular Genetics (Biochemistry
 and Molecular Biophysics); Physiology; Respiratory System (Respiration)
 BIOSYSTEMATIC NAMES: Diptera--Insecta, Arthropoda, Invertebrata, Animalia
 ORGANISMS: Drosophila melanogaster (Diptera)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; arthropods; insects;
 invertebrates
 CHEMICALS & BIOCHEMICALS: BETA-GALACTOSIDASE
 MISCELLANEOUS TERMS: EMBRYONIC DEVELOPMENT; GENE EXPRESSION; GREEN
 FLUORESCENCE PROTEIN; TRACHEAL SYSTEM

CONCEPT CODES:

03506 Genetics and Cytogenetics-Animal
 10300 Replication, Transcription, Translation
 16004 Respiratory System-Physiology and Biochemistry
 25502 Developmental Biology-Embryology-General and Descriptive

64076 Invertebrata, Comparative and Experimental Morphology, Physiology
and Pathology-Insecta-Physiology
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
BIOSYSTEMATIC CODES:

75314 Diptera
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438217 NUCLEAR
297004 LOCALIZATION
343956 SIGNAL
2413566 DETERMIN?
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?s s24 and (reporter or lacz)
5 S24
44730 REPORTER
17783 LACZ
S25 0 S24 AND (REPORTER OR LACZ)

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438217 NUCLEAR
1193985 TRANSPORT
1249469 IDENTIF?
S26 25 NUCLEAR(W)TRANSPORT(3N)IDENTIF?

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...completed examining records
S27 15 RD (unique items)
?s s27 and (reporter or lacz)
15 S27
44730 REPORTER
17783 LACZ
S28 1 S27 AND (REPORTER OR LACZ)
?t/9/all

28/9/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11852619 BIOSIS NO.: 199900098728
Specific binding of the karyopherin Kap121p to a subunit of the nuclear
pore complex containing Nup53p, Nup59p, and Nup170p.
AUTHOR: Marelli Marcello; Aitchison John D; Wozniak Richard W(a)
AUTHOR ADDRESS: (a)Dep. Cell Biol., 5-14 Med. Sci. Build., Univ. Alberta,
Edmonton, AB T6G 2H7*Canada
JOURNAL: Journal of Cell Biology 143 (7):p1813-1830 Dec. 28, 1998
ISSN: 0021-9525
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have identified a specific karyopherin docking complex within
the yeast nuclear pore complex (NPC) that contains two novel,
structurally related nucleoporins, Nup53p and Nup59p, and the NPC core
protein Nup170p. This complex was affinity purified from cells expressing
a functional Nup53p-protein A chimera. The localization of Nup53p,
Nup59p, and Nup170p within the NPC by immunoelectron microscopy suggests
that the Nup53p-containing complex is positioned on both the cytoplasmic
and nucleoplasmic faces of the NPC core. In association with the isolated
complex, we have also *identified* the *nuclear* *transport* factor
Kap121p (Pse1p). Using in vitro binding assays, we showed that each of
the nucleoporins interacts with one another. However, the association of
Kap121p with the complex is mediated by its interaction with Nup53p.
Moreover, Kap121p is the only beta-type karyopherin that binds Nup53p
suggesting that Nup53p acts as a specific Kap121p docking site. Kap121p
can be released from Nup53p by the GTP bound form of the small GTPase
Ran. The physiological relevance of the interaction between Nup53p and
Kap121p was further underscored by the observation that NUP53 mutations
alter the subcellular distribution of Kap121p and the Kap121p-mediated
import of a ribosomal L25 *reporter* protein. Interestingly, Nup53p is
specifically phosphorylated during mitosis. This phenomenon is correlated
with a transient decrease in perinuclear-associated Kap121p.

DESCRIPTORS:

MAJOR CONCEPTS: Cell Biology
BIOSYSTEMATIC NAMES: Fungi--Plantae
ORGANISMS: yeast (Fungi)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Fungi; Microorganisms;
Nonvascular Plants; Plants
CHEMICALS & BIOCHEMICALS: importin; karyopherin; nuclear pore complex;
nuclear transport factor Kap121p; Nup170p; Nup53p; Nup59p
MISCELLANEOUS TERMS: cell cycle; nuclear transport

CONCEPT CODES:

02504 Cytology and Cytochemistry-Plant
03504 Genetics and Cytogenetics-Plant
10060 Biochemical Studies-General
10502 Biophysics-General Biophysical Studies

BIOSYSTEMATIC CODES:

15000 Fungi-Unspecified

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438217 NUCLEAR

1193985 TRANSPORT

46337 SCREEN

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30/1/1 (Item 1 from file: 5)

10710785

?t/9/all

30/9/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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10710785 BIOSIS NO.: 199799331930

GLE2, a *Saccharomyces cerevisiae* homologue of the *Schizosaccharomyces pombe* export factor RAE1, is required for nuclear pore complex structure and function.

AUTHOR: Murphy Robert; Watkins Janis L; Wente Susan R(a)

AUTHOR ADDRESS: (a)Dep. Cell Biol. Physiol., Box 8228, Washington Univ.

Sch. Med., 660 South Euclid Ave., St. Louis*USA

JOURNAL: Molecular Biology of the Cell 7 (12):p1921-1937 1996

ISSN: 1059-1524

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: To identify and characterize novel factors required for *nuclear* *transport*, a genetic *screen* was conducted in the yeast *Saccharomyces cerevisiae*. Mutations that were lethal in combination with a null allele of the gene encoding the nucleoporin Nup100p were isolated using a colony-sectoring assay. Three complementation groups of gle (for GLEF lethal) mutants were identified. In this report, the characterization of GLE2 is detailed. GLE2 encodes a 40.5-kDa polypeptide with striking similarity to that of *Schizosaccharomyces pombe* RAE1. In indirect immunofluorescence and nuclear pore complex fractionation experiments, Gle2p was associated with nuclear pore complexes. Mutated alleles of GLE2 displayed blockage of polyadenylated RNA export; however, nuclear protein import was not apparently diminished. Immunofluorescence and thin-section electron microscopic analysis revealed that the nuclear pore complex and nuclear envelope structure was grossly perturbed in gle2 mutants. Because the clusters of herniated pore complexes appeared subsequent to the export block, the structural perturbations were likely indirect consequences of the export phenotype. Interestingly, a two-hybrid interaction was detected between Gle2p and Srp1p, the nuclear localization signal receptor, as well as Rip1p, a nuclear export signal-interacting protein. We propose that Gle2p has a novel role in mediating nuclear transport.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology;

Membranes (Cell Biology)
 BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae
 ORGANISMS: Saccharomyces cerevisiae (Ascomycetes); Schizosaccharomyces
 pombe (Ascomycetes)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): fungi; microorganisms;
 nonvascular plants; plants
 MISCELLANEOUS TERMS: Research Article; BIOCHEMISTRY AND BIOPHYSICS;
 CELL BIOLOGY; FUNCTION; GLE2; GLE2P; NUCLEAR ENVELOPE; NUCLEAR EXPORT
 SIGNAL-INTERACTING PROTEIN; NUCLEAR LOCALIZATION SIGNAL RECEPTOR;
 NUCLEAR PORE COMPLEX; NUCLEAR TRANSPORT; RAE1; RIP1P; SRP1P; STRUCTURE
 CONCEPT CODES:
 02504 Cytology and Cytochemistry-Plant
 10064 Biochemical Studies-Proteins, Peptides and Amino Acids
 10506 Biophysics-Molecular Properties and Macromolecules
 10508 Biophysics-Membrane Phenomena
 51522 Plant Physiology, Biochemistry and Biophysics-Chemical
 Constituents
 BIOSYSTEMATIC CODES:
 15100 Ascomycetes
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 438217 NUCLEAR
 11728 IMPORT
 1249469 IDENTIF?
 S31 14 NUCLEAR(W)IMPORT(3N)IDENTIF?
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 44730 REPORTER
 17783 LACZ
 S33 5 S9 AND (REPORTER OR LACZ)
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 34/9/1 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
 (c) 2001 BIOSIS. All rts. reserv.

12874064 BIOSIS NO.: 200100081213
 A constitutive region is responsible for nuclear targeting of 4.1R:
 Modulation by alternative sequences results in differential intracellular
 localization.
 AUTHOR: Luque Carlos M; Correas Isabel(a)
 AUTHOR ADDRESS: (a)Centro de Biologia Molecular 'Severo Ochoa' (CSIC/UAM),
 Universidad Autonoma de Madrid, E-28049, Madrid: icorreas@cbm.uam.es**
 Spain
 JOURNAL: Journal of Cell Science 113 (13):p2485-2495 July, 2000
 MEDIUM: print
 ISSN: 0021-9533
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English
 SUMMARY LANGUAGE: English

ABSTRACT: Red blood cell protein 4.1, 4.1R, is an extreme variation on the
 theme of isoform multiplicity. The diverse 4.1R isoforms, mainly
 generated by alternative pre-mRNA splicing, are localized at different
 intracellular sites, including the nucleus. To characterize nonerythroid
 4.1 proteins lacking the most upstream translation initiation site,
 analyze their intracellular localization and define specific domains
 involved in differential intracellular targeting of 4.1R, we cloned 4.1
 cDNAs lacking that translation initiation site. Seven different 4.1R
 cDNAs were isolated. Four of these encoded 4.1R proteins localized
 predominantly to the nucleus and the other three localized to the
 cytoplasm. Three of the nuclear 4.1R isoforms did not contain the
 nuclear *localization* *signal* previously *identified* in the

alternative exon 16. A comparative analysis of the exon composition of the naturally occurring 4.1R cDNAs cloned and of appropriate composite cDNA constructs, with the subcellular distribution of their respective products, demonstrated that a region encoded by constitutive exons, which is therefore common to all 4.1R isoforms and has been termed 'core region', had the capacity of localizing to the nucleus. This region was able to confer nuclear targeting to a cytosolic *reporter*. In protein 4.1R isoforms, the nuclear targeting of the core region is modulated by the expression of alternative exons. Thus, exon 5-encoded sequences eclipsed nuclear entry of the core region, resulting in 4.1R isoforms that predominantly distributed to the cytoplasm. Exon 5 was also able to confer cytoplasmic localization to a nuclear *reporter*. In protein 4.1R isoforms, when exons 5 and 16 were both expressed the nuclear targeting effect of exon 16 was dominant to the inhibitory effect observed by the expression of exon 5, yielding proteins that predominantly localized to the nucleus. Taken together, these results indicate that all 4.1R molecules contain a conserved region that is sufficient to target the protein to the nucleus, but that specific exon-encoded sequences modulate this capacity by acting in a hierarchical order.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology;
Blood and Lymphatics (Transport and Circulation)
BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata,
Animalia
ORGANISMS: MOLT-4 cell line (Hominidae)--human T lymphoid cells
ORGANISMS: PARTS ETC: red blood cell--blood and lymphatics
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Chordates; Humans;
Mammals; Primates; Vertebrates
CHEMICALS & BIOCHEMICALS: 4.1R protein--alternative sequences,
constitutive region, intracellular localization, nuclear targeting, red
blood cell protein

CONCEPT CODES:

02508 Cytology and Cytochemistry-Human
02502 Cytology and Cytochemistry-General
02506 Cytology and Cytochemistry-Animal
10060 Biochemical Studies-General
15002 Blood, Blood-Forming Organs and Body Fluids-Blood and Lymph
Studies
15004 Blood, Blood-Forming Organs and Body Fluids-Blood Cell Studies

BIOSYSTEMATIC CODES:

86215 Hominidae

34/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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12779863 BIOSIS NO.: 200000533486

Gene activation by varicella-zoster virus IE4 protein requires its dimerization and involves both the Arginine-rich sequence, the central part, and the carboxyl-terminal cysteine-rich region.

AUTHOR: Baudoux Laurence; Defechereux Patricia; Rentier Bernard; Piette Jacques(a)

AUTHOR ADDRESS: (a)Laboratory of Fundamental Virology and Immunology,
Institute of Pathology, University of Liege, B23, B-4000, Liege**Belgium
JOURNAL: Journal of Biological Chemistry 275 (42):p32822-32831 October 20,
2000

MEDIUM: print

ISSN: 0021-9258

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: Varicella-zoster virus (VZV) open reading frame 4-encoded protein (IE4) possesses transactivating properties for VZV genes as well as for those of heterologous viruses. Since most transcription factors act as dimers, IE4 dimerization was studied using the mammalian two-hybrid system. Introduction of mutations in the IE4 open reading frame demonstrated that both the central region and the carboxyl-terminal

cysteine-rich domain were important for efficient dimerization. Within the carboxyl-terminal domain, substitution of amino acids encompassing residues 443-447 totally abolished dimerization. Gene activation by IE4 was studied by transient transfection with an IE4 expression plasmid and a *reporter* gene under the control of either the human immunodeficiency virus, type 1, long terminal repeat or the VZV thymidine kinase promoter. Regions of IE4 important for dimerization were also shown to be crucial for transactivation. In addition, the arginine-rich domains Rb and Rc of the amino-terminal region were also demonstrated to be important for transactivation, whereas the Ra domain as well as an acidic and bZIP-containing regions were shown to be dispensable for gene transactivation. A nucleocytoplasmic shuttling of IE4 has also been characterized, involving a *nuclear* *localization* *signal* *identified* within the Rb domain and a nuclear export mechanism partially depending on Crm-1.

REGISTRY NUMBERS: 52-90-4Q: CYSTEINE; 3374-22-9Q: CYSTEINE; 9002-06-6:

THYMIDINE KINASE

DESCRIPTORS:

MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics)

BIOSYSTEMATIC NAMES: Herpesviridae--Animal Viruses, Viruses, Microorganisms; Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae--Animal Viruses, Viruses, Microorganisms

ORGANISMS: HeLa cell line (Hominidae); human immunodeficiency virus-1 (Retroviridae); varicella-zoster virus (Herpesviridae)--pathogen

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

CHEMICALS & BIOCHEMICALS: amino acids; cysteine; plasmids; proteins; *reporter* genes; thymidine kinase--promoter; transcription factors --functions; viral IE4 proteins--analysis, dimerization, functions, molecular regions, nucleocytoplasmic shuttling, structures; viral proteins--analysis, functions

MISCELLANEOUS TERMS: gene mutations; open reading frames; protein nuclear export mechanisms--analysis; viral gene activation mechanisms --analysis; viral genetics

CONCEPT CODES:

10064 Biochemical Studies-Proteins, Peptides and Amino Acids
02508 Cytology and Cytochemistry-Human
03502 Genetics and Cytogenetics-General
03508 Genetics and Cytogenetics-Human
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10802 Enzymes-General and Comparative Studies; Coenzymes
31500 Genetics of Bacteria and Viruses
33506 Virology-Animal Host Viruses

BIOSYSTEMATIC CODES:

02612 Herpesviridae (1993-)
02623 Retroviridae (1993-)
86215 Hominidae

34/9/3 (Item 3 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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09975122 BIOSIS NO.: 199598430040

A polymorphic bipartite motif signals nuclear targeting of early auxin-inducible proteins related to PS-IAA4 from pea (*Pisum sativum*).

AUTHOR: Abel Steffen; Theologis Athanasios(a)

AUTHOR ADDRESS: (a)Plant Gene Expression Cent., 800 Buchanan Street, Albany, CA 94710**USA

JOURNAL: Plant Journal 8 (1):p87-96 1995

ISSN: 0960-7412

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The plant hormone, indoleacetic acid (IAA), transcriptionally activates two early genes in pea, PS-IAA4/5 and PS-IAA6, that encode short-lived nuclear proteins. The identification of the nuclear

localization signals (NLS) in PS-IAA4 and PS-IAA6 using progressive deletion analysis and site-directed mutagenesis is reported. A C-terminal SV40-type NLS is sufficient to direct the beta-glucuronidase *reporter* to the nucleus of transiently transformed tobacco protoplasts, but is dispensable for nuclear localization of both proteins. The dominant and essential NLS in PS-IAA4 and PS-IAA6 overlap with a bipartite basic motif which is polymorphic and conserved in related proteins from other plant species, having the consensus sequence (KKNEK)KR-X-(24-71)-(RSXRK)/(RK/RK). Both basic elements of this motif in PS-IAA4, (KR-X-41-RSYRK), function interdependently as a bipartite NLS. However, in PS-IAA6 (KKNEKKR-X-36-RKK) the upstream element of the corresponding motif contains additional basic residues which allow its autonomous function as an SV40-type monopartite NLS. The spacer-length polymorphism, X-(24-70), in respective bipartite NLS peptides of several PS-IAA4-like proteins from *Arabidopsis thaliana* does not affect nuclear targeting function. The structural and functional variation of the bipartite basic motif in PS-IAA4-like proteins supports the proposed integrated consensus of NLS.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Chemical Coordination and Homeostasis; Genetics; Physiology
 BIOSYSTEMATIC NAMES: Leguminosae--Dicotyledones, Angiospermae, Spermatophyta, Plantae
 ORGANISMS: *Pisum sativum* (Leguminosae)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): angiosperms; dicots; plants; spermatophytes; vascular plants
 MISCELLANEOUS TERMS: FUNCTIONAL VARIATION; GENETIC TRANSFORMATION; *NUCLEAR* *LOCALIZATION* *SIGNAL* *IDENTIFICATION*; PHYTOHORMONE; PROGRESSIVE DELETION ANALYSIS; PS-IAA4-LIKE PROTEINS; SITE-DIRECTED MUTAGENESIS; STRUCTURAL VARIATION

CONCEPT CODES:

02504 Cytology and Cytochemistry-Plant
 03504 Genetics and Cytogenetics-Plant
 10060 Biochemical Studies-General
 10064 Biochemical Studies-Proteins, Peptides and Amino Acids
 10506 Biophysics-Molecular Properties and Macromolecules
 51514 Plant Physiology, Biochemistry and Biophysics-Growth Substances
 51520 Plant Physiology, Biochemistry and Biophysics-Translocation, Accumulation
 51522 Plant Physiology, Biochemistry and Biophysics-Chemical Constituents

BIOSYSTEMATIC CODES:

26260 Leguminosae

34/9/4 (Item 4 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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09765420 BIOSIS NO.: 199598220338

Nucleo-cytoplasmic distribution of human hnRNP proteins: A search for the targeting domains in hnRNP A1.

AUTHOR: Weighardt Florian(a); Biamonti Giuseppe; Riva Silvano

AUTHOR ADDRESS: (a)Ist. Genetica Biochimica Evoluzionistica del, CNR, Univ. degli Studi di Pavia, Via Abbiategrasso **Italy

JOURNAL: Journal of Cell Science 108 (2):p545-555 1995

ISSN: 0021-9533

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: hnRNP A1 (34 kDa) is an RNA binding protein consisting of two tandemly arranged RNA binding domains C-terminally linked to a glycine-rich auxiliary domain (2 times RBDGly). A1 belongs to the set of polypeptides that bind nascent hnRNA in the nucleus to form the so called hnRNP complexes. These complexes seem to be involved both in pre-mRNA processing and in the nuclear export of mRNA. In fact A1, along with other hnRNP proteins, is exported from the nucleus probably bound to mRNA and is immediately re-imported. A1 nuclear re-import, which requires active transcription, is not mediated by a canonical *nuclear*

localization *signal* (NLS). To *identify* the determinants of A1 subcellular localization we developed an expression vector for studying the localization. in transiently transfected cells, of the different structural motifs of A1 fused to a small *reporter* protein (chloramphenicol acetyltransferase, CAT; 26 kDa). We demonstrate that a 30 amino acid sequence in the glycine-rich domain (YNDFGNYNNQSSNFGPMKGGNFGGRSSGPY), which bears no resemblance to canonical NLS, is necessary and sufficient to target the protein to the nucleus. Our data suggest that this targeting sequence might act by mediating the interaction of A1 with a NLS-containing nuclear import complex. On the other hand, the nuclear export of A1 requires at least one RNA binding domain in accord with the hypothesis that A1 exits from the nucleus bound to mRNA. We propose a mechanism for the nucleo-cytoplasmic shuttling of A1 that envisages a specific role for the different structural domains and can explain the dependence of nuclear import from active transcription.

REGISTRY NUMBERS: 9040-07-7: CHLORAMPHENICOL ACETYLTRANSFERASE

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Molecular Genetics (Biochemistry and Molecular Biophysics); Morphology; Physiology

BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGANISMS: Hominidae (Hominidae)

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; humans; mammals; primates; vertebrates

CHEMICALS & BIOCHEMICALS: CHLORAMPHENICOL ACETYLTRANSFERASE

MOLECULAR SEQUENCE DATABANK NUMBER: molecular sequence data; nucleotide sequence

MISCELLANEOUS TERMS: CHLORAMPHENICOL ACETYLTRANSFERASE; HETEROGENEOUS NUCLEAR RNA; MESSENGER RNA; SHUTTLE MECHANISM; TRANSCRIPTION

CONCEPT CODES:

02508 Cytology and Cytochemistry-Human
 03508 Genetics and Cytogenetics-Human
 10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
 10064 Biochemical Studies-Proteins, Peptides and Amino Acids
 10300 Replication, Transcription, Translation
 10506 Biophysics-Molecular Properties and Macromolecules
 10806 Enzymes-Chemical and Physical
 11108 Anatomy and Histology, General and Comparative-Microscopic and Ultramicroscopic Anatomy
 12100 Movement (1971-)
 13012 Metabolism-Proteins, Peptides and Amino Acids
 13014 Metabolism-Nucleic Acids, Purines and Pyrimidines
 10052 Biochemical Methods-Nucleic Acids, Purines and Pyrimidines
 10054 Biochemical Methods-Proteins, Peptides and Amino Acids

BIOSYSTEMATIC CODES:

86215 Hominidae

34/9/5 (Item 5 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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08931054 BIOSIS NO.: 199396082555

The matrix protein of Newcastle disease virus localizes to the nucleus via a bipartite nuclear localization signal.

AUTHOR: Coleman Natalie A; Peeples Mark E(a)

AUTHOR ADDRESS: (a)Dep. Immunol./Microbiol., St. Luke's Med. Cent., 1653 West Congress Parkway, Chicago, IL 60612**USA

JOURNAL: Virology 195 (2):p596-607 1993

ISSN: 0042-6822

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The Newcastle disease virus matrix (M) protein expressed from a cDNA clone is observed in the nucleus of transfected cells, displaying a localization pattern identical to that observed in virus-infected cells.

To *identify* the *nuclear* *localization* *signal* (NLS) in the M protein, M gene mutants encoding deletion and amino acid substitution proteins were constructed and expressed transiently in COS-1 cells. Protein products were examined for intracellular localization using indirect immunofluorescence. Two basic amino acid clusters in the M protein were found to be required for nuclear localization since deletion of these basic clusters or substitution with random amino acids resulted in cytoplasmic localization. Substitution of pairs of basic amino acids with non-basic residues revealed that components from both basic regions are required for nuclear localization. This interdependence between two basic clusters suggests that the NLS in the M protein belongs to the newly described class of "bipartite" NLSs. Unlike most NLSs, M protein sequences containing the critical basic amino acid clusters fused to two different cytoplasmic *reporter* proteins failed to transport these proteins to the nucleus.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Microbiology
 BIOSYSTEMATIC NAMES: Cercopithecidae--Primates, Mammalia, Vertebrata, Chordata, Animalia; Paramyxoviridae--Viruses; Retroviridae--Viruses
 ORGANISMS: simian immunodeficiency virus (Retroviridae); Cercopithecidae (Cercopithecidae); Paramyxoviridae (Paramyxoviridae)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; mammals; microorganisms; nonhuman mammals; nonhuman primates; nonhuman vertebrates; primates; vertebrates; viruses
 MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; molecular sequence data
 MISCELLANEOUS TERMS: CELL TROPISM; ENV GENE; LYMPHOCYTE; MACROPHAGE
 CONCEPT CODES:
 02506 Cytology and Cytochemistry-Animal
 10064 Biochemical Studies-Proteins, Peptides and Amino Acids
 10506 Biophysics-Molecular Properties and Macromolecules
 33506 Virology-Animal Host Viruses
 31500 Genetics of Bacteria and Viruses
 BIOSYSTEMATIC CODES:
 02617 Paramyxoviridae (1993-)
 86205 Cercopithecidae
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S29	2	NUCLEAR(W)TRANSPORT(3N)SCREEN
S30	1	RD (unique items)

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S34      5  RD (unique items)
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      11728  IMPORT
      46337  SCREEN
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      11728  IMPORT
      580197  ASSAY
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      44730  REPORTER
      17783  LACZ
      S38      2  S37 AND(REPORTER OR LACZ)
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39/9/1 (Item 1 from file: 5)
 DIALOG(R)File 5: Biosis Previews(R)
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12639445 BIOSIS NO.: 200000392947
 A genetic system for detection of protein nuclear import and export.
 AUTHOR: Rhee Yoon; Gurel Filiz; Gafni Yedidya; Dingwall Colin; Citovsky
 Vitaly(a)
 AUTHOR ADDRESS: (a)Department of Biochemistry and Cell Biology, Institute
 for Cell and Development Biology, State University of New York, Stony
 Brook, NY, 11794-5215**USA
 JOURNAL: Nature Biotechnology 18 (4):p433-437 April, 2000
 MEDIUM: print
 ISSN: 1087-0156
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English
 SUMMARY LANGUAGE: English

ABSTRACT: We have developed a simple genetic assay to detect active nuclear
 localization (NLS) and export signals (NES) on the basis of their
 function within yeast cells. The bacterial LexA protein was modified
 (mLexA) to abolish its intrinsic NLS and fused to the activation domain
 of the yeast Gal4p (Gal4AD) with or without the SV40 large T-antigen NLS.
 In the import assay, if a tested protein fused to mLexA-Gal4AD contains a
 functional NLS, it will enter the cell nucleus and activate the
 reporter gene expression. In the export assay, if a tested protein
 fused to mLexA-SV40 NLS-Gal4AD contains a functional NES, it will exit
 into the cytoplasm, decreasing the *reporter* gene expression. We tested
 this system with known NLS and NES and then used it to demonstrate a NES
 activity of the capsid protein of a plant geminivirus. This approach may
 help to identify, analyze, and select for proteins containing functional
 NLS and NES.

DESCRIPTORS:

MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular
 Biophysics); Methods and Techniques
 BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae; Geminivirus--Plant
 Viruses, Viruses, Microorganisms; Rhizobiaceae--Gram-Negative Aerobic
 Rods and Cocci, Eubacteria, Bacteria, Microorganisms
 ORGANISMS: Agrobacterium (Rhizobiaceae); Saccharomyces cerevisiae
 (Ascomycetes)--strain-L40; geminivirus (Geminivirus)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Fungi;
 Microorganisms; Nonvascular Plants; Plant Viruses; Plants; Viruses

CHEMICALS & BIOCHEMICALS: LexA protein--nuclear export, nuclear export signal, nuclear import, nuclear localization signal; nucleotoplasmic shuttle protein

METHODS & EQUIPMENT: PCR {polymerase chain reaction}--DNA amplification, amplification method, in-situ recombinant gene expression detection, sequencing techniques; Transformer site-directed mutagenesis kit--Clontech, laboratory equipment; nuclear export assay--Bioassays/Physiological Analysis, analytical method; *nuclear* *import* *assay*--Bioassays/Physiological Analysis, analytical method

CONCEPT CODES:

- 03502 Genetics and Cytogenetics-General
- 03504 Genetics and Cytogenetics-Plant
- 10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
- 31000 Physiology and Biochemistry of Bacteria
- 31500 Genetics of Bacteria and Viruses
- 33508 Virology-Plant Host Viruses

BIOSYSTEMATIC CODES:

- 02816 Geminivirus (1993-)
- 06509 Rhizobiaceae (1992-)
- 15100 Ascomycetes

39/9/2 (Item 2 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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11383718 BIOSIS NO.: 199800165050
 Nuclear import of the capsid protein of tomato yellow leaf curl virus (TYLCV) in plant and insect cells.
 AUTHOR: Kunik Talya; Palanichelvam Karuppaiah; Czosnek Henryk; Citovsky Vitaly; Gafni Yedidya(a)
 AUTHOR ADDRESS: (a)Dep. Genetics, Agric. Res. Organization, PO Box 6, Bet Dagan 50250**Israel
 JOURNAL: Plant Journal 13 (3):p393-399 Feb., 1998
 ISSN: 0960-7412
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: The tomato yellow leaf curl virus (TYLCV) found in Israel is a whitefly-transmitted monopartite geminivirus. Although geminiviruses have been found in the nuclei of phloem-associated cells, the mechanism of viral invasion is poorly understood. The possible role of the TYLCV capsid protein (CP), the only known component of the viral coat, in virus transport into the host cell nucleus was investigated by monitoring its specific nuclear accumulation in plant and insect cells. CP was fused to the beta-glucuronidase (GUS) *reporter* enzyme to *assay* *nuclear* *import* in petunia protoplasts, and micro-injection of purified fluorescently labeled CP was used to examine its nuclear uptake in Drosophila embryos. Both assays demonstrated that TYLCV CP is transported into plant and insect cell nuclei by an active process of nuclear import via a nuclear localization signal (NLS)-specific pathway. Using the GUS assay and deletion analysis, the TYLCV CP NLS sequence was identified in the amino-terminus of the protein.

REGISTRY NUMBERS: 9001-45-0: BETA-GLUCURONIDASE

DESCRIPTORS:

MAJOR CONCEPTS: Infection; Molecular Genetics (Biochemistry and Molecular Biophysics)

BIOSYSTEMATIC NAMES: Diptera--Insecta, Arthropoda, Invertebrata, Animalia ; Geminivirus--Plant Viruses, Viruses, Microorganisms; Solanaceae--Dicotyledones, Angiospermae, Spermatophyta, Plantae

ORGANISMS: petunia (Solanaceae)--protoplasts; tomato yellow leaf curl virus {TYLCV} (Geminivirus); Drosophila (Diptera)

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Angiosperms; Animals; Arthropods; Dicots; Insects; Invertebrates; Microorganisms; Plant Viruses; Plants; Spermatophytes; Vascular Plants; Viruses

CHEMICALS & BIOCHEMICALS: capsid protein

METHODS & EQUIPMENT: beta-glucuronidase assay method--genetic method

MISCELLANEOUS TERMS: nuclear import

CONCEPT CODES:

31500 Genetics of Bacteria and Viruses
 33508 Virology-Plant Host Viruses
 54510 Phytopathology-Diseases Caused by Viruses
 BIOSYSTEMATIC CODES:
 02816 Geminivirus (1993-)
 26775 Solanaceae
 75314 Diptera

?ds

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S6	71	RD (unique items)
S7	0	S6 AND LACZ
S8	5	S6 AND REPORTER
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S37	26	RD (unique items)
S38	2	S37 AND (REPORTER OR LACZ)
S39	2	RD (unique items)

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 624355 MODIF?
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 438217 NUCLEAR
 297004 LOCALIZATION
 343956 SIGNAL
 2766 NUCLEAR(W)LOCALIZATION(W)SIGNAL
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 S42 2 RD (unique items)
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42/3/1 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
 (c) 2001 BIOSIS. All rts. reserv.

12639445 BIOSIS NO.: 200000392947
 A genetic system for detection of protein nuclear import and export.
 AUTHOR: Rhee Yoon; Gurel Filiz; Gafni Yedidya; Dingwall Colin; Citovsky Vitaly(a)
 AUTHOR ADDRESS: (a)Department of Biochemistry and Cell Biology, Institute for Cell and Development Biology, State University of New York, Stony Brook, NY, 11794-5215*+USA
 JOURNAL: Nature Biotechnology 18 (4):p433-437 April, 2000
 MEDIUM: print
 ISSN: 1087-0156
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English
 SUMMARY LANGUAGE: English

42/3/2 (Item 1 from file: 155)
 DIALOG(R)File 155:MEDLINE(R)

10803379 99242601 PMID: 10225947
 Phosphorylation regulates in vivo interaction and molecular targeting of serine/arginine-rich pre-mRNA splicing factors.
 Yeakley JM; Tronchere H; Olesen J; Dyck JA; Wang HY; Fu XD
 Division of Cellular and Molecular Medicine, Department and School of Medicine, University of California, San Diego, La Jolla, California 92093-0651, USA.
 Journal of cell biology (UNITED STATES) May 3 1999, 145 (3) p447-55,
 ISSN 0021-9525 Journal Code: HMV
 Languages: ENGLISH
 Document type: Journal Article
 Record type: Completed
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S7	0	S6 AND LACZ
S8	5	S6 AND REPORTER
S9	5	RD (unique items)
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S28	1	S27 AND (REPORTER OR LACZ)
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S35	0	NUCLEAR(W)IMPORT(3N)SCREEN
S36	43	NUCLEAR(W)IMPORT(3N)ASSAY
S37	26	RD (unique items)

S38 2 S37 AND(REPORTER OR LACZ)
 S39 2 RD (unique items)
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 11728 IMPORT
 1566330 DETEC?
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 ...completed examining records
 S44 3 RD (unique items)
 ?t/3/all

44/3/1 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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12787454 BIOSIS NO.: 200000541077
 Positive injury signals induce growth and prolong survival in Aplysia
 neurons.
 AUTHOR: Zhang Xiao-Ping; Ambron Richard T(a)
 AUTHOR ADDRESS: (a)Department of Anatomy and Cell Biology, Columbia
 University, W. 168th Street, 1204 Black Building, New York, NY, 10032+
 USA
 JOURNAL: Journal of Neurobiology 45 (2):p84-94 November 5, 2000
 MEDIUM: print
 ISSN: 0022-3034
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English
 SUMMARY LANGUAGE: English

44/3/2 (Item 2 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
 (c) 2001 BIOSIS. All rts. reserv.

12639445 BIOSIS NO.: 200000392947
 A genetic system for *detection* of protein *nuclear* *import* and export.
 AUTHOR: Rhee Yoon; Gurel Filiz; Gafni Yedidya; Dingwall Colin; Citovsky
 Vitaly(a)
 AUTHOR ADDRESS: (a)Department of Biochemistry and Cell Biology, Institute
 for Cell and Development Biology, State University of New York, Stony
 Brook, NY, 11794-5215+*USA
 JOURNAL: Nature Biotechnology 18 (4):p433-437 April, 2000
 MEDIUM: print
 ISSN: 1087-0156
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English
 SUMMARY LANGUAGE: English

44/3/3 (Item 3 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
 (c) 2001 BIOSIS. All rts. reserv.

12362230 BIOSIS NO.: 200000115732
 Diminished human immunodeficiency virus type 1 reverse transcription and
 nuclear transport in primary macrophages arrested in early G1 phase of
 the cell cycle.
 AUTHOR: Kootstra Neeltje A; Zwart Bianca M; Schuitemaker Hanneke(a)
 AUTHOR ADDRESS: (a)Dept. of Clinical Viral-Immunology, Central Laboratory
 of the Netherlands Red Cross Blood Transfusion Service, Plesmanlaan 125,
 1066 CX, Amsterdam*+Netherlands
 JOURNAL: Journal of Virology 74 (4):p1712-1717 Feb., 2000
 ISSN: 0022-538X
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract

LANGUAGE: English
SUMMARY LANGUAGE: English
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11728 IMPORT
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17783 LACZ
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49/3/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

12073184 BIOSIS NO.: 199900368033
Enhancement of polylysine-mediated transferrin infection by nuclear
localization sequences: Polylysine does not function as a nuclear
localization sequence.
AUTHOR: Chan Chee Kai; Jans David A(a)
AUTHOR ADDRESS: (a)Nuclear Signalling Laboratory, Division for Biochemistry
and Molecular Biology, John Curtin Scho**Australia
JOURNAL: Human Gene Therapy 10 (10):p1695-1702 July 1, 1999
ISSN: 1043-0342
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

49/3/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

09304821 BIOSIS NO.: 199497313191
A ligand-dependent bipartite nuclear targeting signal in the human androgen
receptor: Requirement for the DNA-binding domain and modulation by
NH-2-terminal and carboxyl-terminal sequences.
AUTHOR: Zhou Zhong-Xun; Sar Madhabananda; Simental Jorge A; Lane Malcolm V;
Wilson Elizabeth M(a)
AUTHOR ADDRESS: (a)Lab. Reprod. Biol., CB 7500 ManNider Bldg., Univ. North
Carolina, Chapel Hill, NC 27599**USA
JOURNAL: Journal of Biological Chemistry 269 (18):p13115-13123 1994
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
?t/9/2

49/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts..reserv.

09304821 BIOSIS NO.: 199497313191
A ligand-dependent bipartite nuclear targeting signal in the human androgen
receptor: Requirement for the DNA-binding domain and modulation by
NH-2-terminal and carboxyl-terminal sequences.

AUTHOR: Zhou Zhong-Xun; Sar Madhabananda; Simental Jorge A; Lane Malcolm V;
 Wilson Elizabeth M(a)
 AUTHOR ADDRESS: (a)Lab. Reprod. Biol., CB 7500 ManNider Bldg., Univ. North
 Carolina, Chapel Hill, NC 27599*USA
 JOURNAL: Journal of Biological Chemistry 269 (18):p13115-13123 1994
 ISSN: 0021-9258
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: The amino acid sequence requirements for androgen-dependent androgen receptor *nuclear* *import* were *determined* by immunostaining transiently expressed full-length wild-type and mutant human androgen receptors (AR) in monkey kidney COS cells and measuring transcriptional activity by cotransfection with a luciferase *reporter* vector in monkey kidney CV1 cells. Mutagenesis studies revealed a bipartite nuclear targeting sequence in the DNA binding and hinge regions at amino acids 617-633, consisting of two clusters of basic amino acids separated by 10 amino acids, RKCYEAGMTLGARKLKK. In a series of deletion mutants, AR NH-2-terminal fragments (residues 1-639 through 1-723) displayed constitutive nuclear import, and transcriptional activity was similar to that of the ligand-activated full-length wild type AR. In contrast, nuclear import and transcriptional activation were inhibited by sequence extensions into the steroid-binding domain (1-771). Constitutive nuclear import was regained in part by NH-2-terminal deletions of full-length AR. Expression of AR/pyruvate kinase chimeras defined a sequence required for predominant nuclear localization as residues 580-661, comprised of the second zinc finger region of the DNA-binding domain, the 17-amino-acid putative targeting sequence, and 28 residues of flanking carboxyl-terminal sequence. These studies suggest that the bipartite nuclear targeting sequence of AR includes flanking sequence and is modulated by interactions between the NH-2- and carboxyl-terminal regions.

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Endocrine System
 (Chemical Coordination and Homeostasis); Genetics; Reproductive System
 (Reproduction)
 BIOSYSTEMATIC NAMES: Hominidae--Primates, Mammalia, Vertebrata, Chordata,
 Animalia
 ORGANISMS: Hominidae (Hominidae)
 BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; chordates; humans;
 mammals; primates; vertebrates
 MISCELLANEOUS TERMS: AMINO-TERMINAL SEQUENCE; GENE REGULATION;
 MOLECULAR SEQUENCE

CONCEPT CODES:

03508 Genetics and Cytogenetics-Human
 10067 Biochemical Studies-Sterols and Steroids
 10506 Biophysics-Molecular Properties and Macromolecules
 16504 Reproductive System-Physiology and Biochemistry
 17006 Endocrine System-Gonads and Placenta

BIOSYSTEMATIC CODES:

86215 Hominidae

?ds

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S5	124	NUCLEAR(W)LOCALIZATION(W)SIGNAL(2N)IDENTIF?
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S8	5	S6 AND REPORTER
S9	5	RD (unique items)
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S15	12	RD (unique items)

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S40     104  LEXA(S) (DELETE? OR MODIF?)
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$0.00    1 Type(s) in Format 1
$24.75   15 Type(s) in Format 3
$44.55   27 Type(s) in Format 9
$69.30   43 Types
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$1.75 TYMNET
$113.68 Estimated cost this search
$113.91 Estimated total session cost 6.812 DialUnits

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Status: Signed Off. (36 minutes)